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OM protein - protein search, using sw model

Run on: June 6, 2006, 22:41:51 ; Search time 16 Seconds
(without alignments)
321.656 Million cell updates/sec

Title: US-10-063-537-32

Perfect score: 445

Sequence: 1 MSGRDTILGLIALALSIA.....QQDKHSIRNEEGTELOAIVR 445

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 59871 seqs, 11565156 residues

Word size : 6

Total number of hits satisfying chosen parameters: 222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New,*

- 1: /EMC_Celerra_SID33/prodata/2/pubpaa/US09_NEW_PUB.pbp.*
- 2: /EMC_Celerra_SID33/prodata/2/pubpaa/US06_NEW_PUB.pbp.*
- 3: /EMC_Celerra_SID33/prodata/2/pubpaa/US07_NEW_PUB.pbp.*
- 4: /EMC_Celerra_SID33/prodata/2/pubpaa/US08_NEW_PUB.pbp.*
- 5: /EMC_Celerra_SID33/prodata/2/pubpaa/PCT_NEW_PUB.pbp.*
- 6: /EMC_Celerra_SID33/prodata/2/pubpaa/US10_NEW_PUB.pbp.*
- 7: /EMC_Celerra_SID33/prodata/2/pubpaa/US11_NEW_PUB.pbp.*
- 8: /EMC_Celerra_SID33/prodata/2/pubpaa/US60_NEW_PUB.pbp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	445	100.0	445	6	US-10-196-749-148 Sequence 148, App
2	445	100.0	445	7	US-11-101-316-32 Sequence 32, Appl
3	8	1.8	184	6	US-10-953-349-34460 Sequence 34460, A
4	7	1.6	134	6	US-10-953-349-30350 Sequence 30350, A
5	7	1.6	213	7	US-11-293-697-4111 Sequence 4111, Ap
6	7	1.6	218	6	US-10-953-349-22764 Sequence 22764, A
7	7	1.6	332	6	US-10-953-349-10360 Sequence 10360, A
8	7	1.6	357	6	US-10-953-349-10359 Sequence 10359, A
9	7	1.6	368	6	US-10-953-349-22763 Sequence 22763, A
10	7	1.6	391	6	US-10-953-349-22762 Sequence 22762, A
11	7	1.6	405	6	US-10-953-349-3312 Sequence 3312, Ap
12	7	1.6	468	6	US-10-511-937-2595 Sequence 2595, Ap
13	7	1.6	469	6	US-10-953-349-3311 Sequence 3311, Ap
14	7	1.6	471	6	US-10-953-349-10358 Sequence 10358, A
15	7	1.6	496	6	US-10-953-349-3310 Sequence 3310, Ap
16	7	1.6	1122	6	US-10-953-349-7840 Sequence 7840, Ap
17	7	1.6	1147	6	US-10-953-349-7839 Sequence 7839, Ap
18	7	1.6	1211	6	US-10-953-349-7838 Sequence 7838, Ap
19	6	1.3	9	7	US-11-140-487A-1382 Sequence 1382, Ap
20	6	1.3	10	7	US-11-140-487A-1149 Sequence 1149, Ap
21	6	1.3	10	7	US-11-140-487A-1187 Sequence 1187, Ap
22	6	1.3	10	7	US-11-140-487A-1267 Sequence 1267, Ap
23	6	1.3	10	7	US-11-140-487A-1383 Sequence 1383, Ap
24	6	1.3	15	7	US-11-140-487A-2169 Sequence 2169, Ap
25	6	1.3	62	6	US-10-953-349-18220 Sequence 18220, A

RESULT 1

US-10-196-749-148
; Sequence 148, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 148
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-148

ALIGNMENTS

Sequence 34566, A
Sequence 10513, A
Sequence 18287, A
Sequence 3382, Ap
Sequence 30729, A
Sequence 2685, Ap
Sequence 37632, A
Sequence 12880, A
Sequence 20413, A
Sequence 37586, A
Sequence 8614, Ap
Sequence 10512, A
Sequence 2323, Ap
Sequence 28044, A
Sequence 37631, A
Sequence 12279, A
Sequence 18286, A
Sequence 3328, Ap
Sequence 8613, Ap
Sequence 25282, A

US-10-953-349-34566
US-10-953-349-10513
US-10-953-349-18287
US-11-293-697-3382
US-10-953-349-30729
US-11-293-697-2685
US-10-953-349-37632
US-10-953-349-12280
US-10-953-349-20413
US-10-953-349-37586
US-10-953-349-8614
US-10-953-349-10512
US-10-953-349-2323
US-10-953-349-28044
US-10-953-349-37631
US-10-953-349-12279
US-10-953-349-18286
US-11-293-697-3328
US-10-953-349-8613
US-10-953-349-25282

26 6 1.3 78 6
27 6 1.3 81 6
28 6 1.3 105 6
29 6 1.3 105 7
30 6 1.3 109 6
31 6 1.3 111 7
32 6 1.3 112 6
33 6 1.3 113 6
34 6 1.3 113 6
35 6 1.3 113 6
36 6 1.3 114 6
37 6 1.3 118 6
38 6 1.3 119 6
39 6 1.3 119 6
40 6 1.3 119 6
41 6 1.3 120 6
42 6 1.3 120 6
43 6 1.3 120 7
44 6 1.3 122 6
45 6 1.3 124 6

Query Match 100.0%; Score 445; DB 6; Length 445;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGRDILGICILALALSAMMTFFRITLLVHIFISLVILGLFVCGVLMWLYDYTN 60
DB 1 MSGRDILGICILALALSAMMTFFRITLLVHIFISLVILGLFVCGVLMWLYDYTN 60

QY 61 DLSIEDTERENMKCVLGFPAIVSTGITAVLLVLI FVLRKRIKLTVELFOITNKAISSAPF 120
DB 61 DLSIEDTERENMKCVLGFPAIVSTGITAVLLVLI FVLRKRIKLTVELFOITNKAISSAPF 120

QY 121 LFPQPLWTFAILIFFVWLWAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMMSYHLIGLI 180
DB 121 LFPQPLWTFAILIFFVWLWAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMMSYHLIGLI 180

QY 181 WTSEFILACQOMTIAGAVVTCYFNRSKNDDPPDHPILSSLSILFFYHQGTVVKGSFLISVV 240
DB 181 WTSEFILACQOMTIAGAVVTCYFNRSKNDDPPDHPILSSLSILFFYHQGTVVKGSFLISVV 240

QY 241 RIPRIIVMYMQUALKEQOHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300
DB 241 RIPRIIVMYMQUALKEQOHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300

QY 301 TSAKDAFKILSKNSSHTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPL 360
DB 301 TSAKDAFKILSKNSSHTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPL 360

QY 361 LLVAFAYLVAHSFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKL 420
DB 361 LLVAFAYLVAHSFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKL 420

QY 421 NNARAQODKHSRLNREGTELOAIVR 445
DB 421 NNARAQODKHSRLNREGTELOAIVR 445

RESULT 2
US-11-101-316-32
; Sequence 32, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 32
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo Sapien

US-11-101-316-32

Query Match 100.0%; Score 445; DB 7; Length 445;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGRDILGICILALALSAMMTFFRITLLVHIFISLVILGLFVCGVLMWLYDYTN 60
DB 1 MSGRDILGICILALALSAMMTFFRITLLVHIFISLVILGLFVCGVLMWLYDYTN 60

QY 61 DLSIEDTERENMKCVLGFPAIVSTGITAVLLVLI FVLRKRIKLTVELFOITNKAISSAPF 120
DB 61 DLSIEDTERENMKCVLGFPAIVSTGITAVLLVLI FVLRKRIKLTVELFOITNKAISSAPF 120

QY 121 LFPQPLWTFAILIFFVWLWAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMMSYHLIGLI 180
DB 121 LFPQPLWTFAILIFFVWLWAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMMSYHLIGLI 180

QY 181 WTSEFILACQOMTIAGAVVTCYFNRSKNDDPPDHPILSSLSILFFYHQGTVVKGSFLISVV 240
DB 181 WTSEFILACQOMTIAGAVVTCYFNRSKNDDPPDHPILSSLSILFFYHQGTVVKGSFLISVV 240

QY 241 RIPRIIVMYMQUALKEQOHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300
DB 241 RIPRIIVMYMQUALKEQOHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300

QY 301 TSAKDAFKILSKNSSHTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPL 360
DB 301 TSAKDAFKILSKNSSHTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPL 360

QY 361 LLVAFAYLVAHSFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKL 420
DB 361 LLVAFAYLVAHSFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQEFLSFVKRSNKL 420

QY 421 NNARAQODKHSRLNREGTELOAIVR 445
DB 421 NNARAQODKHSRLNREGTELOAIVR 445

RESULT 3
US-10-953-349-34460
; Sequence 34460, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 34460
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays

US-10-953-349-34460

Query Match 1.8%; Score 8; DB 6; Length 184;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 357 AVPLLLVA 364
DB 122 AVPLLLVA 129

RESULT 4
US-10-953-349-30350
; Sequence 30350, Application US/109533349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30350
; LENGTH: 134
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-30350

Query Match 1.6%; Score 7; DB 6; Length 134;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 112 NKAISSA 118
Db 5 NKAISSA 11
|||||

RESULT 5
US-11-293-697-4111
; Sequence 4111, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/11/293,697
; CURRENT FILING DATE: 2005-12-05
; PRIOR APPLICATION NUMBER: US/10/108,260
; PRIOR FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4111
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4111

Query Match 1.6%; Score 7; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 ILGLLFV 47
Db 43 ILGLLFV 49
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RESULT 6
US-10-953-349-22764
; Sequence 22764, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22764
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22764

Query Match 1.6%; Score 7; DB 6; Length 218;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 TVVKGSGF 235
|||||

Db 113 TVVKGSGF 119

RESULT 7

US-10-953-349-10360
; Sequence 10360, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10360
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10360

Query Match 1.6%; Score 7; DB 6; Length 332;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CILALAL 17
Db 135 CILALAL 141
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RESULT 8

US-10-953-349-10359
; Sequence 10359, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 10359
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-10359

Query Match 1.6%; Score 7; DB 6; Length 357;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CILALAL 17
Db 160 CILALAL 166
|||||

RESULT 9

US-10-953-349-22763
; Sequence 22763, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22763

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; LENGTH: 368
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22763

Query Match          1.6%; Score 7; DB 6; Length 368;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 TVVKGSP 235
Db 263 TVVKGSP 269

RESULT 10
US-10-953-349-22762
; Sequence 22762, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22762
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22762

Query Match          1.6%; Score 7; DB 6; Length 391;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 229 TVVKGSP 235
Db 286 TVVKGSP 292

RESULT 11
US-10-953-349-3312
; Sequence 3312, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3312
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3312

Query Match          1.6%; Score 7; DB 6; Length 405;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CILALAL 17
Db 202 CILALAL 208

RESULT 12
US-10-511-937-2595
; Sequence 2595, Application US/10511937
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; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2595
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2595

Query Match          1.6%; Score 7; DB 6; Length 468;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 358 VPLLVA 364
Db 250 VPLLVA 256

RESULT 13
US-10-953-349-3311
; Sequence 3311, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3311
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3311

Query Match          1.6%; Score 7; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 CILALAL 17
Db 266 CILALAL 272

RESULT 14
US-10-953-349-10358
; Sequence 10358, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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; TITLE OF INVENTION: ENCODED THERBY
 ; FILE REFERENCE: 2750-1579FUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 10358
 ; LENGTH: 471
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-10-953-349-10358

Query Match 1.6%; Score 7; DB 6; Length 471;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CILALAL 17
 Db 274 CILALAL 280

RESULT 15
 US-10-953-349-3310
 ; Sequence 3310, Application US/10953349
 ; Publication No. US20060107345A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ALEXANDROV, Nikolai et al.
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
 ; FILE REFERENCE: 2750-1579FUS2
 ; CURRENT APPLICATION NUMBER: US/10/953,349
 ; CURRENT FILING DATE: 2004-09-30
 ; NUMBER OF SEQ ID NOS: 40252
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 3310
 ; LENGTH: 496
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 US-10-953-349-3310

Query Match 1.6%; Score 7; DB 6; Length 496;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CILALAL 17
 Db 293 CILALAL 299

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(without alignments)
1126.397 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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741	445	100.0	445	5	US-10-972-317-32
743	445	100.0	445	5	US-10-950-374-177
751	445	100.0	445	6	US-11-102-240-32
752	445	100.0	445	6	US-11-103-195-32
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754	344	77.3	653	4	US-10-391-399-73
755	310	69.7	648	5	US-10-330-773-825
756	215	48.3	275	3	US-09-833-245-1911
757	125	28.4	275	6	US-11-264-096-1911
758	122	27.4	275	3	US-09-833-245-1910
759	122	27.4	275	6	US-11-264-096-1910
760	34	7.6	46	4	US-10-425-115-336095
761	27	6.1	558	5	US-10-330-773-822
762	23	5.2	94	4	US-10-425-115-280712
763	23	5.2	329	4	US-10-220-120-317
764	18	4.0	646	4	US-10-062-937B-10
765	18	4.0	646	4	US-10-391-399-78
766	11	2.5	301	5	US-10-745-586-174
767	11	2.5	446	3	US-09-726-643-58
768	11	2.5	446	3	US-10-042-141-58
769	11	2.5	446	5	US-10-919-272-58
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771	11	2.5	510	4	US-10-042-141-139
772	11	2.5	510	5	US-10-919-272-139
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777	11	2.5	657	4	US-10-176-847-48	Sequence 48, Appl
778	11	2.5	657	5	US-10-753-267-6	Sequence 6, Appl
779	11	2.5	657	6	US-11-080-991-48	Sequence 48, Appl
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783	8	1.8	13	5	US-10-671-317-20	Sequence 20, Appl
784	8	1.8	15	4	US-10-430-685-130	Sequence 130, App
785	8	1.8	24	6	US-11-064-039-27	Sequence 27, Appl
786	8	1.8	24	6	US-11-065-970-39	Sequence 39, Appl
787	8	1.8	24	6	US-11-167-636-39	Sequence 39, Appl
788	8	1.8	35	5	US-10-816-768-3	Sequence 3, Appl
789	8	1.8	70	4	US-10-425-115-216147	Sequence 216147,
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791	8	1.8	103	3	US-09-754-831A-12	Sequence 12, Appl
792	8	1.8	103	4	US-10-187-394-11	Sequence 11, Appl
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795	8	1.8	103	6	US-11-037-782-164	Sequence 164, App
796	8	1.8	103	6	US-11-097-960-72	Sequence 72, Appl
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798	8	1.8	104	3	US-09-852-318A-26	Sequence 26, Appl
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806	8	1.8	119	4	US-10-154-333-18	Sequence 18, Appl
807	8	1.8	119	4	US-10-704-223-16	Sequence 16, Appl
808	8	1.8	120	3	US-09-813-459-16	Sequence 16, Appl
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810	8	1.8	120	3	US-09-880-708-20	Sequence 20, Appl
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832	8	1.8	472	5	US-10-942-042-8	Sequence 8, Appl
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845	8	1.8	1023	6	US-11-045-004-894	Sequence 894, App
846	8	1.8	1045	3	US-09-815-242-10617	Sequence 10617, A

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848	8	1.8	2424	6	US-11-097-143-3564	Sequence 3564, Ap	921	7	1.6	150	4	US-10-424-599-232173	Sequence 232173, A
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854	7	1.6	27	6	US-11-129-741-640	Sequence 640, App	927	7	1.6	165	4	US-10-767-701-35659	Sequence 35659, A
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858	7	1.6	43	3	US-09-305-736-433	Sequence 433, App	931	7	1.6	174	4	US-10-767-701-42635	Sequence 42635, A
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860	7	1.6	43	3	US-09-818-683-433	Sequence 433, App	933	7	1.6	176	5	US-10-774-355A-2402	Sequence 2402, Ap
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862	7	1.6	47	5	US-10-935-098-80	Sequence 80, Appl	935	7	1.6	182	4	US-10-767-701-36313	Sequence 36313, A
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892	7	1.6	106	6	US-11-096-568A-27368	Sequence 27368, A	965	7	1.6	240	5	US-10-864-252-552	Sequence 552, App
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999	7	1.6	310	4	US-10-027-801-44	Sequence 44, Appl	1072	7	1.6	466	4	US-10-425-114-54986	Sequence 54986, A
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1002	7	1.6	320	4	US-10-024-399-8	Sequence 8, Appli	1075	7	1.6	466	6	US-11-087-099-11198	Sequence 11198, A
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1005	7	1.6	324	6	US-11-188-298-20130	Sequence 20130, A	1078	7	1.6	467	4	US-10-280-047-6	Sequence 6, Appli
1006	7	1.6	328	4	US-10-425-115-27313	Sequence 27313, A	1079	7	1.6	467	6	US-11-185-878-6	Sequence 6, Appli
1007	7	1.6	331	4	US-10-425-114-56240	Sequence 56240, A	1080	7	1.6	468	4	US-10-226-296-2	Sequence 2, Appli
1008	7	1.6	333	4	US-10-425-114-57911	Sequence 57911, A	1081	7	1.6	468	4	US-10-226-318-2	Sequence 2, Appli
1009	7	1.6	335	5	US-10-467-657-1466	Sequence 1466, Ap	1082	7	1.6	468	4	US-10-175-902-2	Sequence 2, Appli
1010	7	1.6	336	6	US-11-188-298-11778	Sequence 11778, A	1083	7	1.6	468	4	US-10-322-673-1	Sequence 1, Appli
1011	7	1.6	340	4	US-10-128-714-8089	Sequence 8089, Ap	1084	7	1.6	468	4	US-10-139-785-1	Sequence 1, Appli
1012	7	1.6	340	4	US-10-425-114-52527	Sequence 52527, A	1085	7	1.6	468	4	US-10-292-486-1	Sequence 1, Appli
1013	7	1.6	340	6	US-11-096-568A-22078	Sequence 22078, A	1086	7	1.6	468	4	US-10-333-712-2	Sequence 2, Appli
1014	7	1.6	341	4	US-10-032-585-7491	Sequence 7491, Ap	1087	7	1.6	468	4	US-10-660-128-1	Sequence 1, Appli
1015	7	1.6	351	4	US-10-425-114-67931	Sequence 67931, A	1088	7	1.6	468	4	US-10-437-963-163502	Sequence 163502,
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1017	7	1.6	353	5	US-10-732-923-7920	Sequence 7920, Ap	1090	7	1.6	468	4	US-10-480-730-1	Sequence 1, Appli
1018	7	1.6	354	5	US-10-467-657-5634	Sequence 5634, Ap	1091	7	1.6	468	4	US-10-630-329-2	Sequence 2, Appli
1019	7	1.6	358	4	US-10-425-115-193071	Sequence 193071, A	1092	7	1.6	468	4	US-10-491-326-3	Sequence 3, Appli
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1024	7	1.6	369	4	US-10-128-714-3374	Sequence 3374, Ap	1097	7	1.6	468	5	US-10-981-621-1	Sequence 1, Appli
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1028	7	1.6	375	5	US-10-506-454-606	Sequence 606, App	1101	7	1.6	468	5	US-10-986-376-1	Sequence 1, Appli
1029	7	1.6	377	4	US-10-369-493-1482	Sequence 1482, Ap	1102	7	1.6	468	5	US-10-995-561-907	Sequence 907, App
1030	7	1.6	377	4	US-10-425-115-302079	Sequence 302079, A	1103	7	1.6	468	6	US-11-076-187-2	Sequence 2, Appli
1031	7	1.6	382	4	US-10-128-714-8374	Sequence 8374, Ap	1104	7	1.6	468	6	US-11-221-281-1	Sequence 1, Appli
1032	7	1.6	391	4	US-10-289-762-364	Sequence 364, App	1105	7	1.6	471	4	US-10-424-599-253079	Sequence 253079,
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1038	7	1.6	404	6	US-11-096-568A-22077	Sequence 22077, A	1111	7	1.6	479	5	US-10-450-763-33014	Sequence 33014, A
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1054	7	1.6	424	5	US-10-732-923-22223	Sequence 22223, A	1127	7	1.6	501	5	US-10-472-928-3536	Sequence 3536, Ap
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1059	7	1.6	438	4	US-10-425-114-45307	Sequence 45307, A	1132	7	1.6	518	6	US-11-127-939-48	Sequence 48, Appl
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1146	7	1.6	559	4	US-10-050-704-111	Sequence 111, App	1219	7	1.6	1280	4	US-10-101-433A-3	Sequence 3, Appli
1147	7	1.6	559	4	US-10-798-512-111	Sequence 111, App	1220	7	1.6	1280	4	US-10-619-359A-2	Sequence 2, Appli
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1160	7	1.6	640	4	US-10-127-032-138	Sequence 138, App	1233	6	1.3	8	6	US-11-045-024-4385	Sequence 4385, Ap
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1170	7	1.6	725	4	US-10-437-963-103774	Sequence 103774,	1243	6	1.3	9	4	US-10-107-533-682	Sequence 682, App
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1172	7	1.6	770	4	US-10-437-963-181869	Sequence 181869,	1245	6	1.3	9	4	US-10-107-533-1216	Sequence 1216, Ap
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1174	7	1.6	799	4	US-10-425-114-52019	Sequence 52019, A	1247	6	1.3	9	4	US-10-107-533-1748	Sequence 1748, Ap
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1176	7	1.6	802	6	US-10-282-122A-60651	Sequence 60651, A	1249	6	1.3	9	4	US-10-107-533-2292	Sequence 2292, Ap
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1178	7	1.6	804	6	US-11-097-143-32436	Sequence 32436, A	1251	6	1.3	9	4	US-10-107-533-2883	Sequence 2883, Ap
1179	7	1.6	820	5	US-10-450-763-54183	Sequence 54183, A	1252	6	1.3	9	4	US-10-107-533-2883	Sequence 2883, Ap
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1181	7	1.6	822	6	US-11-188-298-6572	Sequence 6572, Ap	1254	6	1.3	9	4	US-10-107-533-4413	Sequence 4413, Ap
1182	7	1.6	833	4	US-10-369-493-14004	Sequence 14004, A	1255	6	1.3	9	4	US-10-107-533-4571	Sequence 4571, Ap
1183	7	1.6	833	4	US-10-282-122A-68007	Sequence 68007, A	1256	6	1.3	9	4	US-10-107-533-4597	Sequence 4597, Ap
1184	7	1.6	857	3	US-09-970-944-36	Sequence 36, Appl	1257	6	1.3	9	6	US-10-107-533-4639	Sequence 4639, Ap
1185	7	1.6	857	4	US-10-099-322-133	Sequence 133, App	1258	6	1.3	9	6	US-11-045-024-1913	Sequence 1913, Ap
1186	7	1.6	857	4	US-10-044-564-133	Sequence 133, App	1259	6	1.3	9	6	US-11-045-024-1914	Sequence 1914, Ap
1187	7	1.6	857	6	US-11-054-281-133	Sequence 133, App	1260	6	1.3	9	6	US-11-045-024-1915	Sequence 1915, Ap
1188	7	1.6	862	3	US-09-738-626-3956	Sequence 3956, Ap	1261	6	1.3	9	6	US-11-045-024-4512	Sequence 4512, Ap
1189	7	1.6	862	5	US-10-494-672-308	Sequence 308, App	1262	6	1.3	9	6	US-11-045-024-4513	Sequence 4513, Ap
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1191	7	1.6	884	4	US-10-437-963-158195	Sequence 158195,	1264	6	1.3	9	6	US-11-045-024-5852	Sequence 5852, Ap
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1193	7	1.6	891	4	US-10-424-599-184810	Sequence 184810,	1266	6	1.3	9	6	US-11-045-024-7833	Sequence 7833, Ap
1194	7	1.6	894	5	US-10-732-923-8428	Sequence 8428, Ap	1267	6	1.3	10	3	US-09-755-630A-73	Sequence 73, Appl
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1197	7	1.6	923	4	US-10-174-677-95	Sequence 95, Appl	1270	6	1.3	10	4	US-10-200-708-464	Sequence 464, App
1198	7	1.6	923	4	US-10-174-677-96	Sequence 96, Appl	1271	6	1.3	10	4	US-10-107-533-463	Sequence 463, App
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Query Match      100.0%; Score 445; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 2
US-09-990-444-177
; Sequence 177, Application US/09990444
; Patent No. 6930170
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: KJavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C19
; CURRENT APPLICATION NUMBER: US/09/990,444
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
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 ; PRIOR FILING DATE: 1998-07-07
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 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 445; DB 2; Length 445;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB	1	MSGRDTILGCTILALSLAMMFTFRFITTLLVHIFISLIVILGLLFVCGVLMWLYDYTN	60
QY	61	DSIELDTERENMKCVLGFVSTGITAVLLVLI FVLRKRKIKLTVELFQITNKAISSAPF	120
DB	61	DSIELDTERENMKCVLGFVSTGITAVLLVLI FVLRKRKIKLTVELFQITNKAISSAPF	120
QY	121	LLFQPLWTFALLIFFWVLWVAVLLSGTAGAAQVMEGGQVEYKPLSGIRYMMSYHLIGLI	180
DB	121	LLFQPLWTFALLIFFWVLWVAVLLSGTAGAAQVMEGGQVEYKPLSGIRYMMSYHLIGLI	180
QY	181	WTSEFILACQOMTIAGAVTTCYENRSKNDDPPDHPILSSLSILFFVHQGTWVKGSELI SVV	240
DB	181	WTSEFILACQOMTIAGAVTTCYENRSKNDDPPDHPILSSLSILFFVHQGTWVKGSELI SVV	240
QY	241	RIPRIIVMTQMALKBOQHGSRLFRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC	300
DB	241	RIPRIIVMTQMALKBOQHGSRLFRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC	300
QY	301	TSAKDAFKILSKNSSHFTSINCFDPIIFLGKVLVVCFTVFGGLMAFNVRAPQVWAVPL	360
DB	301	TSAKDAFKILSKNSSHFTSINCFDPIIFLGKVLVVCFTVFGGLMAFNVRAPQVWAVPL	360
QY	361	LLVAFAYLVAHSFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQSEFLSFVKRSNKL	420
DB	361	LLVAFAYLVAHSFLSVFETVLDALFLCFAVDLETNDGSSEKPYFMDQSEFLSFVKRSNKL	420
QY	421	NNARAQODKHSRLNREBGTLEQAIVR	445
DB	421	NNARAQODKHSRLNREBGTLEQAIVR	445

RESULT 3
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 ; Sequence 177, Application US/09997333
 ; Patent No. 6953836
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David	PRIOR APPLICATION NUMBER: 60/088202
APPLICANT: Desnoyers, Luc	PRIOR FILING DATE: 1998-06-05
APPLICANT: Eaton, Dan L.	PRIOR APPLICATION NUMBER: 60/088212
APPLICANT: Ferrara, Napoleone	PRIOR FILING DATE: 1998-06-05
APPLICANT: Fong, Sherman	PRIOR APPLICATION NUMBER: 60/088217
APPLICANT: Gerber, Hanspeter	PRIOR FILING DATE: 1998-06-05
APPLICANT: Gerritsen, Mary E.	PRIOR APPLICATION NUMBER: 60/088655
APPLICANT: Goddard, Audrey	PRIOR FILING DATE: 1998-06-09
APPLICANT: Godowski, Paul J.	PRIOR APPLICATION NUMBER: 60/088734
APPLICANT: Grimaldi, J. Christopher	PRIOR FILING DATE: 1998-06-10
APPLICANT: Gurney, Austin L.	PRIOR APPLICATION NUMBER: 60/088738
APPLICANT: Kljavin, Ivar J.	PRIOR FILING DATE: 1998-06-10
APPLICANT: Napier, Mary A.	PRIOR APPLICATION NUMBER: 60/088742
APPLICANT: Pan, James	PRIOR FILING DATE: 1998-06-10
APPLICANT: Paoni, Nicholas F.	PRIOR APPLICATION NUMBER: 60/088810
APPLICANT: Roy, Margaret Ann	PRIOR FILING DATE: 1998-06-10
APPLICANT: Stewart, Timothy A.	PRIOR APPLICATION NUMBER: 60/088824
APPLICANT: Tumas, Daniel	PRIOR FILING DATE: 1998-06-10
APPLICANT: Watanabe, Colin K.	PRIOR APPLICATION NUMBER: 60/088826
APPLICANT: Williams, P. Mickey	PRIOR FILING DATE: 1998-06-10
APPLICANT: Wood, William I.	PRIOR APPLICATION NUMBER: 60/088858
APPLICANT: Zhang, Zemin	PRIOR FILING DATE: 1998-06-11
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic	
FILE REFERENCE: P2730PIC27	
CURRENT APPLICATION NUMBER: US/09/997,333	
CURRENT FILING DATE: 2001-11-15	
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 445; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 LLFQPLMTFAILLFFWVLWVAVLLSLGTAGAAQVMGGQVEYKPLSGIRYMWYHLIGLI 180
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QY 181 WTSEFILAQQMTITAGAVVTCYFNRSKNDDPDHPILSSLSILFFYHOGTVVKGSLISVV 240
Db 181 WTSEFILAQQMTITAGAVVTCYFNRSKNDDPDHPILSSLSILFFYHOGTVVKGSLISVV 240

QY 241 RIPRIIWMQNALKEQHGALSRFLRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300
Db 241 RIPRIIWMQNALKEQHGALSRFLRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300

QY 301 TSAKDAFKILSKNSGHFTSINCFGDFIIFLGLKVLVVCFTVFGGLMAFNYNRAFOVWAVPL 360
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QY 361 LLVAFFAVLVAHSFLSVFETVLDLFLCFVAVDLETNDSSEKPYFMDQBFLSFVKRSNKL 420
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QY 421 NNARAQQDKHSLRNEBEGTELOAIVR 445
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RESULT 4
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; Sequence 177, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deshoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
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; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087607
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; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759


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Db 61 DLSIEDLTRENKMCVLGFAIVSTGTAVALVLI FVLRKRIKLTVELFOITNKAISSAPP 120
QY 121 LIFQPLWTFAILTFVFWLVAVALLSLGTAGAAQVMGGQVEYKPLSGIRYMSYHLIGLI 180
Db 121 LIFQPLWTFAILTFVFWLVAVALLSLGTAGAAQVMGGQVEYKPLSGIRYMSYHLIGLI 180
QY 181 WTSEFILACQOMTIAGAVTCTYFNRSKNPPDPHPILSSLSILFFYHQGTWVGSLISVV 240
Db 181 WTSEFILACQOMTIAGAVTCTYFNRSKNPPDPHPILSSLSILFFYHQGTWVGSLISVV 240
QY 241 RPIRIIVMYMNAKKEQOHCALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFC 300
Db 241 RPIRIIVMYMNAKKEQOHCALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFC 300
QY 301 TSAKDAFKILSNSSHFTSINCFGDFIIFLGKLVVVCFTVFGGLMAFNYNRAFAQWAVPL 360
Db 301 TSAKDAFKILSNSSHFTSINCFGDFIIFLGKLVVVCFTVFGGLMAFNYNRAFAQWAVPL 360
QY 361 LLVAFAYILVAHSFLSVFETVLDALFLCFADVLETNDGSSSEKPYFMDQBFSLSPVKRSNKL 420
Db 361 LLVAFAYILVAHSFLSVFETVLDALFLCFADVLETNDGSSSEKPYFMDQBFSLSPVKRSNKL 420
QY 421 NNARAQODKHSURNESGTLEQATVR 445
Db 421 NNARAQODKHSURNESGTLEQATVR 445
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RESULT 5

US-09-989-735-177
; Sequence 177, Application US/09989735
; Patent No. 6972185

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C61
; CURRENT APPLICATION NUMBER: US/09/989, 735
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/087827  
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 Qy 121 LLFQPLWTFAILIFFWVWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLI 180
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 Qy 241 RIPRIIWMYQNALKEQOQHAGLSRYLPRCCYCCFWCLDKYLLHLNQAYTTTAINGTDFC 300
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 ; Patent No. 7018811
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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39 PRIOR FILING DATE: 1998-07-09

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; PRIOR FILING DATE: 1998-07-09

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Query Match 100.0%; Score 445; DB 3; Length 445;
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Db 61 DLSIELDTERENMKCVLGEAIVSTGITAVLLVLI FVLKRKIKLTVELFOITNKAISSAPF 120
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RESULT 8

US-09-989-728-177

; Sequence 177, Application US/09989728

; Patent No. 7029873

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
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; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
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 ; PRIOR FILING DATE: 1998-07-09
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RESULT 9

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 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
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 ; APPLICANT: Fong, Sherman
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 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C37
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; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090535
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; PRIOR APPLICATION NUMBER: 60/090696
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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 445; DB 3; Length 445;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSGRDTILGCIILALALSLAMMTEFTITLLVHFIFISLVILGLLFCVGLWMLYYDTN 60

Db 1 MSGRDTILGCIILALALSLAMMTEFTITLLVHFIFISLVILGLLFCVGLWMLYYDTN 60

Qy 61 DLSIELDTERENMKCVLGFVAVSTGITAVALLVILFVLKRIKLTVELFQITNKAISSAPF 120

Db 61 DLSIELDTERENMKCVLGFVAVSTGITAVALLVILFVLKRIKLTVELFQITNKAISSAPF 120

Qy 121 LLFQPLWTFAILFFVWLVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWVSHLIGLI 180

Db 121 LLFQPLWTFAILFFVWLVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWVSHLIGLI 180

Qy 181 WTSEFTILACQOMTIAGAVTTCYFNRSKNDDPPDHPILSSLSILFFYHOGTVVKGSLISVV 240

Db 181 WTSEFTILACQOMTIAGAVTTCYFNRSKNDDPPDHPILSSLSILFFYHOGTVVKGSLISVV 240

Qy 241 RIPRIIWMYMONALKEOQHGAISRYLPRCCYCCFWCLDKYLLHUNQAYTTTALNGTDFC 300

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Db 241 RIPRIIWMYQNALKEQQHGALSRYLPRCCYCCFCWCLDKYLLHLNQNAYTITTTAINGTDFC 300
QY 301 TSADAFKILSKNSSHTSINCGDFIIFLGKVLVVCFTVFGGIMAFNYNRAFOQWAVPL 360
Db 301 TSADAFKILSKNSSHTSINCGDFIIFLGKVLVVCFTVFGGIMAFNYNRAFOQWAVPL 360
QY 361 LLVAFAYLVAHFSFLSVFETVLDAFLCFPAVDLETNDGSGSEKPYFMDQDFLSFVKESNKL 420
Db 361 LLVAFAYLVAHFSFLSVFETVLDAFLCFPAVDLETNDGSGSEKPYFMDQDFLSFVKESNKL 420
QY 421 NNAAQODKXSLRNEGTLEQAIVR 445
Db 421 NNAAQODKXSLRNEGTLEQAIVR 445

RESULT 11
US-09-989-293A-177
; Sequence 177, Application US/09989293A
; Patent No. 7034136
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989,293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
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; PRIOR APPLICATION NUMBER: 60/088861
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089908


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; FILING DATE: 29-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 103,604
; FILING DATE: 06-AUG-1993
; APPLICATION NUMBER: 827,052
; FILING DATE: 28-JAN-1992
; APPLICATION NUMBER: 579,865
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: 179,406
; FILING DATE: 08-APR-1988
; SEQ ID NO:6:
; LENGTH: 12
5496552-6

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Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      217 SSLSILFF 224
Db      2 SSLSILFF 9

RESULT 14
US-09-374-958C-3
; Sequence 3, Application US/09374958C
; Patent No. 6677432
; GENERAL INFORMATION:
; APPLICANT: Stryker Corporation
; TITLE OF INVENTION: Modified Proteins and DNAs of the TGF-beta Superfamily, Including
; TITLE OF INVENTION: Modified Morphogenic Proteins
; FILE REFERENCE: STK-076
; CURRENT APPLICATION NUMBER: US/09/374,958C
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 3
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: BMP-3
US-09-374-958C-3

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Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      217 SSLSILFF 224
Db      6 SSLSILFF 13

RESULT 15
US-09-374-936-3
; Sequence 3, Application US/09374936
; Patent No. 6846906
; GENERAL INFORMATION:
; APPLICANT: Oppermann, Hermann
; APPLICANT: Tai, Mei-Sheng
; APPLICANT: McCartney, John
; TITLE OF INVENTION: Modified TGF-beta Superfamily Proteins
; FILE REFERENCE: STK-077
; CURRENT APPLICATION NUMBER: US/09/374,936
; CURRENT FILING DATE: 1999-08-16
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: BMP-3

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US-09-374-936-3

Query Match      1.8%; Score 8; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      217 SSLSILFF 224
Db      6 SSLSILFF 13

Search completed: June  6, 2006, 22:31:03
Job time : 52 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 6, 2006, 22:21:11 ; Search time 297 Seconds
(without alignments)
1385.966 Million cell updates/sec

Title: US-10-063-537-32
Perfect score: 445
Sequence: 1 MSGRDTILGLCILALSLA.....QQDKHSLNBEGETLOAIVR 445

Scoring table:
OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2849598 seqs, 925015592 residues

Word size : 6

Total number of hits satisfying chosen parameters: 29628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : UniProt 7.2.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	344	77.3	605	2	Q726C5_HUMAN	Q726C5 homo sapien
2	344	77.3	653	1	CTL3_HUMAN	Q8n4m1 homo sapien
3	27	6.1	652	1	CTL3_MOUSE	Q921v7 mus musculus
4	23	5.2	604	1	CTL3_RAT	Q6ay92 rattus norv
5	18	4.0	646	1	CTL1_TORMA	Q9i9b9 torpedo mar
6	18	4.0	651	2	Q63253_XENLA	Q63253 xenopus lae
7	18	4.0	651	2	Q6IR74_XENLA	Q6IR74 xenopus lae
8	11	2.5	94	2	Q4T3N9_TETNG	Q4T3N9 tetraodon n
9	11	2.5	653	1	CTL1_MOUSE	Q6x893 mus musculus
10	11	2.5	656	1	CTL1_RAT	Q8vi16 rattus norv
11	11	2.5	657	1	CTL1_HUMAN	Q8wvi5 homo sapien
12	10	2.2	677	2	Q7Q5E7_ANOGA	Q7Q5E7 anopheles g
13	9	2.0	155	2	Q4H957_9DEIO	Q4H957 deinoceroc
14	9	2.0	263	2	Q9A2U8_CAUCR	Q9A2U8 caulobacter
15	8	1.8	77	2	Q74K77_LACJO	Q74K77 lactobacill
16	8	1.8	77	2	Q8A2U7_BACTN	Q8A2U7 bacteroides
17	8	1.8	85	2	Q4CLR3_TREYCR	Q4CLR3 trypanosoma
18	8	1.8	109	2	Q6MX36_MYCTU	Q6MX36 mycobacteri
19	8	1.8	109	2	Q7U1W5_MYCBO	Q7U1W5 mycobacteri
20	8	1.8	114	1	PD211_FIG	Q6itq4 sus scrofa
21	8	1.8	117	2	Q9NSW2_CABEL	Q9NSW2 caenorhabdi
22	8	1.8	128	2	Q8QFL3_ONCMV	Q8QFL3 oncorhynch
23	8	1.8	132	2	Q3QZG3_XYLEFA	Q3QZG3 xylella fas
24	8	1.8	132	2	Q3R644_XYLEFA	Q3R644 xylella fas
25	8	1.8	132	2	Q3RH12_XYLEFA	Q3RH12 xylella fas
26	8	1.8	132	2	Q87DE9_XYLEFT	Q87DE9 xylella fas
27	8	1.8	132	2	Q9PD58_XYLEFA	Q9PD58 xylella fas
28	8	1.8	133	2	Q3Z8F4_DEHEL	Q3Z8F4 dehalococco
29	8	1.8	147	1	LYSC3_SHEEP	Q9tun1 ovis aries
30	8	1.8	152	1	M440_ARATH	P93300 arabidopsis
31	8	1.8	152	2	Q6DR78_ARATH	Q6DR78 arabidopsis

32	8	1.8	157	2	Q8XRT5_RALSO	Q8xrt5 ralstonia s
33	8	1.8	161	2	Q50GJ6_9BACT	Q50GJ6 uncultured
34	8	1.8	161	2	Q3SJ19_THIDA	Q3sej19 thiobacillu
35	8	1.8	162	2	Q67KS7_SYMTH	Q67ks7 symbiobacte
36	8	1.8	163	2	Q50GJ4_9BACT	Q50gJ4 uncultured
37	8	1.8	163	2	Q50GJ5_9BACT	Q50gJ5 uncultured
38	8	1.8	163	2	Q50GJ7_9BACT	Q50gJ7 uncultured
39	8	1.8	163	2	Q50GJ8_9BACT	Q50gJ8 uncultured
40	8	1.8	163	2	Q50GJ9_9BACT	Q50gJ9 uncultured
41	8	1.8	167	2	Q9UIR9_CABEL	Q9uiR9 caenorhabdi
42	8	1.8	175	2	Q4X0Y5_ASPFU	Q4x0Y5 aspergillus
43	8	1.8	177	2	Q2LI72_9GAMM	Q2li72 crenothrix
44	8	1.8	181	2	Q33X89_9GAMM	Q33x89 shewanella
45	8	1.8	188	2	Q4A884_MYCH7	Q4a884 mycoplasma

ALIGNMENTS

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AC	Q726C5;	integrated into UniProtKB/TrEMBL.		
DT	01-OCT-2003,	sequence version 1.		
DT	01-OCT-2003,	entry version 12.		
DE	Hypothetical protein SLC44A3.			
DE	Hypothetical protein SLC44A3.			
GN	Name=SLC44A3;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Colon;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RC	TISSUE=Colon;			
RG	NIH MGC Project;			
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms			
CC	Distributed under the Creative Commons Attribution-NoDerivs License			
CC	-----			
DR	EMBL; BC053877; AAH53877.1; -; mRNA.			
DR	Ensembl; ENSG00000143036; Homo sapiens.			
DR	LinkHub; Q726C5; -			
DR	InterPro; IPR007603; DUF580.			
DR	PANTHER; PTHR12385; DUF580; 1.			
DR	Pfam; PF04515; DUF580; 1.			
KW	Hypothetical protein.			

SQ SEQUENCE 605 AA; 68047 MW; 1182534F9556DADD CRC64;

Query Match 77.3%; Score 344; DB 2; Length 605;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSGRDITLGLCTIALALSAMMPTFRFTITLLVHIFISVLGLLFCVGLWLVYDYTN 60
 DB 161 MSGRDITLGLCTIALALSAMMPTFRFTITLLVHIFISVLGLLFCVGLWLVYDYTN 220

QY 61 DLSIELDTERENKCVLGFALVSTGITAVLLVLI FVLKRKIKLTVELFOITNKAISSAPP 120
 DB 221 DLSIELDTERENKCVLGFALVSTGITAVLLVLI FVLKRKIKLTVELFOITNKAISSAPP 280

QY 121 LFPQPLWTFAILFFVWLVAVLLSGLTAGAAWEGGVQVEKPLSGIRYMSYHLIGLI 180
 DB 281 LFPQPLWTFAILFFVWLVAVLLSGLTAGAAWEGGVQVEKPLSGIRYMSYHLIGLI 340

QY 181 WTSEFILACQOMTIAGAVTVCYENRKNDDPDHPILSSLSILFFYHOGTVWKGSLISVV 240
 DB 341 WTSEFILACQOMTIAGAVTVCYENRKNDDPDHPILSSLSILFFYHOGTVWKGSLISVV 400

QY 241 RIPRIIVMYMNAKQEQHAGLSRYLFRCCYCCFWCLDKYLLHLNQAVYTTTAINGTDFC 300
 DB 401 RIPRIIVMYMNAKQEQHAGLSRYLFRCCYCCFWCLDKYLLHLNQAVYTTTAINGTDFC 460

QY 301 TSAKDAFKILSKNSHTSINCSDGFIIFLGLKVLVCFVFGGLMAFNYNRAFOVWAVPL 360
 DB 461 TSAKDAFKILSKNSHTSINCSDGFIIFLGLKVLVCFVFGGLMAFNYNRAFOVWAVPL 520

QY 361 LLVAFAYLVAHGFSLVFETVLDALFLCFADLETNDGSGSEKPYFMDQBFSLSPVKRSNKL 420
 DB 521 LLVAFAYLVAHGFSLVFETVLDALFLCFADLETNDGSGSEKPYFMDQBFSLSPVKRSNKL 580

QY 421 NNARAQDKHSLNREGTELQAIVR 445
 DB 581 NNARAQDKHSLNREGTELQAIVR 605

RESULT 2

CTL3_HUMAN ID_CTL3_HUMAN STANDARD; PRT; 653 AA.
 AC Q8N4W1; Q6UWT1; Q9BWY7;
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 30-AUG-2005, sequence version 3.
 DT 07-MAR-2006, entry version 15.
 DE Choline transporter-like protein 3 (Solute carrier family 44 member 3).
 GN Name=SLC44A3; Synonyms=CTL3; ORFNames=UNQ558/PRO1115;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RG Human chromosome 1 international sequencing consortium;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Brain, and Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong F.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshlyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 147-653, AND VARIANT
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K.I., Baldwin D.T., Brush J.,
 RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
 RA Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heidens S.,
 RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
 RA Lewis L., Liao D., Mark M.R., Robbie E., Sanchez C., Schoenfeld J.,
 RA Seshagiri S., Simmons L., Watanabe C., Smith J., Stinson J., Vagts A.,
 RA Vandlen R.L., Wamande C., Wieand D., Woods K., Xie M.-H.,
 RA Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D.,
 RA Wood W.I., Godowski P.J., Gray A.M.,
 RT "The secreted protein discovery initiative (SPDI), a large-scale
 RT effort to identify novel human secreted and transmembrane proteins: a
 RT bioinformatics assessment.";
 RL Genome Res. 13:2265-2270(2003).
 RN [4]
 RP IDENTIFICATION, AND NOMENCLATURE.
 RX MEDLINE=20144127; PubMed=10677542; DOI=10.1073/pnas.030339697;
 RA O'Regan S., Traifford E., Ruat M., Cha N., Compaore D., Meunier P.-M.;
 RT "An electric lobe suppressor for a yeast choline transporter mutation
 RT belongs to a new family of transporter-like proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1835-1840(2000).
 CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
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EMBL; AC093429; -; NOT ANNOTATED CDS; Genomic DNA.
 DR EMBL; AL359554; CAC36091.1; -; Genomic DNA.
 DR EMBL; BC033858; AAH3858.2; ALT INIT; mRNA.
 DR EMBL; AY358659; AAQ89022.1; ALT INIT; mRNA.
 DR Ensembl; ENSG0000143036; Homo sapiens.
 DR HGNC; HGNC:28689; SLC44A3.
 DR InterPro; IPR007603; DUF580.
 DR Pfam; PF04515; DUF580; 1.
 KW Membrane; Polymorphism; Transmembrane.
 FT CHAIN 1 653
 FT /FTID=PRO_0000191720.
 FT TRANSMEM 34 54 Potential.
 FT TRANSMEM 213 233 Potential.
 FT TRANSMEM 243 263 Potential.
 FT TRANSMEM 284 304 Potential.
 FT TRANSMEM 334 354 Potential.
 FT TRANSMEM 384 404 Potential.
 FT TRANSMEM 428 448 Potential.
 FT TRANSMEM 534 554 Potential.
 FT TRANSMEM 563 583 Potential.
 FT VARIANT 438 438 I -> V (in dbSNP:rs59098).
 FT /FTID=VAR_023405.
 FT CONFLICT 465 465 Missing (in Ref. 1; CAC36091).
 FT SEQUENCE 653 AA; 73797 MW; 54807C920086427B CRC64;

Query Match 77.3%; Score 344; DB 1; Length 653;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 444; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSGRDITLGLCTIALALSAMMPTFRFTITLLVHIFISVLGLLFCVGLWLVYDYTN 60
 DB 209 MSGRDITLGLCTIALALSAMMPTFRFTITLLVHIFISVLGLLFCVGLWLVYDYTN 268

QY 61 DLSIEDTERENKCVGLFAIVSTGTAVALLVLI FVLKRIKLTVELFQITNKAISSAPP 120
 DLSIEDTERENKCVGLFAIVSTGTAVALLVLI FVLKRIKLTVELFQITNKAISSAPP 328
 DLSIEDTERENKCVGLFAIVSTGTAVALLVLI FVLKRIKLTVELFQITNKAISSAPP 328
 QY 121 LFPQPLWTFALLFFVWLVAVLLSGTAGAAQVMEGGQVEYKPLSGIRVWMSYHLIGLI 180
 LFPQPLWTFALLFFVWLVAVLLSGTAGAAQVMEGGQVEYKPLSGIRVWMSYHLIGLI 180
 LFPQPLWTFALLFFVWLVAVLLSGTAGAAQVMEGGQVEYKPLSGIRVWMSYHLIGLI 388
 LFPQPLWTFALLFFVWLVAVLLSGTAGAAQVMEGGQVEYKPLSGIRVWMSYHLIGLI 388
 QY 181 WTSEFLIACQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTGVKGSFLISVV 240
 WTSEFLIACQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTGVKGSFLISVV 240
 WTSEFLIACQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTGVKGSFLISVV 448
 WTSEFLIACQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTGVKGSFLISVV 448
 QY 241 RPIRIIVMYQNALKEQHQALSGRYLPRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300
 RPIRIIVMYQNALKEQHQALSGRYLPRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300
 RPIRIIVMYQNALKEQHQALSGRYLPRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 508
 RPIRIIVMYQNALKEQHQALSGRYLPRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 508
 QY 301 TSAKDAFKILSKSSSHTSINCFDGFIFLFGKLVLCFTVFGGLMAFNYNRAQVWAVPL 360
 TSAKDAFKILSKSSSHTSINCFDGFIFLFGKLVLCFTVFGGLMAFNYNRAQVWAVPL 360
 TSAKDAFKILSKSSSHTSINCFDGFIFLFGKLVLCFTVFGGLMAFNYNRAQVWAVPL 568
 TSAKDAFKILSKSSSHTSINCFDGFIFLFGKLVLCFTVFGGLMAFNYNRAQVWAVPL 568
 QY 361 LLVAFAYLVHVSFLSFVETVLDALFLCFAVDLETNDGSSSEKPYFMDQEFSLFVKS NKL 420
 LLVAFAYLVHVSFLSFVETVLDALFLCFAVDLETNDGSSSEKPYFMDQEFSLFVKS NKL 420
 LLVAFAYLVHVSFLSFVETVLDALFLCFAVDLETNDGSSSEKPYFMDQEFSLFVKS NKL 628
 LLVAFAYLVHVSFLSFVETVLDALFLCFAVDLETNDGSSSEKPYFMDQEFSLFVKS NKL 628
 QY 421 NNARAQDKHSLRNEEGTELOAIVR 445
 NNARAQDKHSLRNEEGTELOAIVR 445
 NNARAQDKHSLRNEEGTELOAIVR 653
 NNARAQDKHSLRNEEGTELOAIVR 653

RESULT 3
 CTL3_MOUSE STANDARD; PRT; 652 AA.
 ID CTL3_MOUSE
 AC Q921V7
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 30-AUG-2005, sequence version 2.
 DT 07-MAR-2006, entry version 27.
 DE Choline transporter-like protein 3 (Solute carrier family 44 member 3).
 DE 3).
 GN Name=Slc44a3; Synonyms=Ctl3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -i- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By similarity).
 CC -i- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
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 CC

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 CC
 DR EMBL; BC010552; AAH10552.1; ALT INIT; mRNA.
 DR EMBL; BC025548; AAH25548.1; ALT INIT; mRNA.
 DR Ensembl; ENSMUSG00000039865; Mus musculus.
 DR MGI; MGI:2384860; Slc44a3.
 DR InterPro; IPR007603; DUF580.
 DR Pfam; PF04515; DUF580; 1.
 KW Membrane; Transmembrane.
 FT CHAIN 1 652
 FT TRANSMEM 33 53
 FT TRANSMEM 212 232
 FT TRANSMEM 238 258
 FT TRANSMEM 284 304
 FT TRANSMEM 333 353
 FT TRANSMEM 377 397
 FT TRANSMEM 533 553
 FT TRANSMEM 562 582
 SQ SEQUENCE 652 AA; 73028 MW; A0DA359C7509C8B3 CRC64;
 Choline transporter-like protein 3.
 /FTid=PRO_0000191721.
 Query Match 6.1%; Score 27; DB 1; Length 652;
 Best Local Similarity 100.0%; Pred. No. 1.2e-16;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 37 ISLVILGLLFCVGLVWLVVYDYNDLS 63
 ISLVILGLLFCVGLVWLVVYDYNDLS 63
 DB 244 ISLVILGLLFCVGLVWLVVYDYNDLS 270
 RESULT 4
 CTL3_RAT STANDARD; PRT; 604 AA.
 ID CTL3_RAT
 AC Q6AY32;
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 13-SEP-2004, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE Choline transporter-like protein 3 (Solute carrier family 44 member 3).
 DE 3).
 GN Name=Slc44a3; Synonyms=Ctl3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Kidney;
 RG NIH - Mammalian Gene Collection (MGC) project;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP TISSUE SPECIFICITY.
 RC STRAIN=Wistar; TISSUE=Brain;
 RX PubMed=15715662; DOI=10.1111/j.1471-4159.2004.02962.x;
 RA Traiffort E., Ruat M., O'Regan S., Meunier F.-M.,
 RA "Molecular characterization of the family of choline transporter-like proteins and their splice variants."
 RT J. Neurochem. 92:1116-1125(2005).
 RL J. Neurochem. 92:1116-1125(2005).
 CC -i- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By similarity).
 CC -i- TISSUE SPECIFICITY: Expressed in colon, kidney and ileum.
 CC -i- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
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 CC
 DR EMBL; BC079142; AAH79142.1; -; mRNA.
 DR RGD; 1305808; Ctl3.
 DR InterPro; IPR007603; DUF580.
 DR PANTHER; PTHR12385; DUF580; 1.
 DR Pfam; PF04515; DUF580; 1.
 KW Membrane; Transmembrane.
 FT CHAIN 1 604
 Choline transporter-like protein 3.

FT TRANSMEM 165 185 /FtId=PRO_0000191722.
 FT TRANSMEM 195 215 Potential.
 FT TRANSMEM 237 257 Potential.
 FT TRANSMEM 286 306 Potential.
 FT TRANSMEM 330 350 Potential.
 FT TRANSMEM 485 505 Potential.
 FT TRANSMEM 514 534 Potential.
 SQ SEQUENCE 604 AA; 67679 MW; BA7C3A411CE3E1B CRC64;

Query Match 5.2%; Score 23; DB 1; Length 604;
 Best Local Similarity 100.0%; Pred. No. 8.6e-13;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 LFLCFAVDLETNDGSSSKPYFMD 407
 Db 544 LFLCFAVDLETNDGSSSKPYFMD 566
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RESULT 5

CTLI_TORMA STANDARD; PRT; 646 AA.
 AC Q91B9;
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-2000, sequence version 1.
 DT 07-FEB-2006, entry version 17.
 DE Choline transporter-like protein 1.
 GN Name=CTLI;
 OS Torpedo marmorata (Marbled electric ray).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Squala; Hypnosqualea; Pristiorajae; Batoidae;
 OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
 OX NCBI_TaxID=7788;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA], AND FUNCTION.
 RX MEDLINE=20144127; PubMed=10677542; DOI=10.1073/pnas.030339697;
 RA O'Regan S., Traffort E., Ruat M., Cha N., Compaore D., Meunier F.-M.;
 RT "An electric lobe suppressor for a yeast choline transport mutation
 belongs to a new family of transporter-like proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1835-1840(2000).
 RN [2]
 RP TISSUE SPECIFICITY, AND SUBCELLULAR LOCATION.
 RX PubMed=12352613; DOI=10.1097/00001756-200209160-00009;
 RA Meunier F.-M., O'Regan S.;
 RT "Expression of CTLI in myelinating structures of Torpedo marmorata.";
 RL NeuroReport 13:1617-1620(2002).
 RN [3]
 RP FUNCTION, AND TISSUE SPECIFICITY.
 RX PubMed=12675144; DOI=10.1023/A:1022877524469;
 RA O'Regan S., Meunier F.-M.;
 RT "Selection and characterization of the choline transport mutation
 suppressor from Torpedo electric lobe, CTLI.";
 RL Neurochem. Res. 28:551-555(2003).
 CC -1- FUNCTION: Probable choline transporter. May be involved in
 membrane synthesis and myelin production.
 CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
 CC -1- TISSUE SPECIFICITY: Present in myelinating structures from brain
 and spinal chord (at protein level).
 CC -1- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
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 CC -----
 DR ENBL; A0245618; CAB75556.1; -; mRNA.
 DR InterPro; IPR007603; DUF580.
 DR PANTHER; PTHR12385; DUF580; 1.
 DR Pfam; PF04515; DUF580; 1.
 KM Membrane; Transmembrane; Transport.
 FT CHAIN 1 646 Choline transporter-like protein 1.
 FT /FtId=PRO_0000191715.
 FT TOPO_DOM 1 27 Cytoplasmic (Potential).
 FT TRANSMEM 28 48 Potential.
 FT TOPO_DOM 49 207 Extracellular (Potential).

FT TRANSMEM 208 228 Potential.
 FT TOPO_DOM 229 233 Cytoplasmic (Potential).
 FT TRANSMEM 234 254 Potential.
 FT TOPO_DOM 255 281 Extracellular (Potential).
 FT TRANSMEM 282 302 Potential.
 FT TOPO_DOM 303 308 Cytoplasmic (Potential).
 FT TRANSMEM 309 329 Potential.
 FT TOPO_DOM 330 331 Extracellular (Potential).
 FT TRANSMEM 332 352 Potential.
 FT TOPO_DOM 353 373 Cytoplasmic (Potential).
 FT TRANSMEM 374 394 Potential.
 FT TOPO_DOM 395 435 Extracellular (Potential).
 FT TRANSMEM 436 456 Potential.
 FT TOPO_DOM 457 530 Cytoplasmic (Potential).
 FT TRANSMEM 531 551 Potential.
 FT TOPO_DOM 552 559 Extracellular (Potential).
 FT TRANSMEM 560 580 Potential.
 FT TOPO_DOM 581 646 Cytoplasmic (Potential).
 FT COMPLETAS 467 485 Cys-rich.
 SQ SEQUENCE 646 AA; 72254 MW; A19A0E1D81453F6F CRC64;
 Query Match 4.0%; Score 18; DB 1; Length 646;
 Best Local Similarity 100.0%; Pred. No. 6.3e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 183 SEFILACQQTITAGAVVT 200
 Db 389 SEFILACQQTITAGAVVT 406
 |||||

RESULT 6
 Q63ZS3 XENLA PRELIMINARY; PRT; 651 AA.
 ID Q63ZS3_XENLA
 AC Q63ZS3;
 DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 25-OCT-2004, sequence version 1.
 DT 07-FEB-2006, entry version 10.
 DE MGC82240 protein.
 GN Name=MGC82240;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Splice;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Splice;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Gernhard D.S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
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CC
CC
DR EMBL; BC082837; AAH82837.1; -; mRNA.
DR InterPro; IPR007603; DUF580.
DR PANTHER; PTHR12385; DUF580; 1.
DR Pfam; PF04515; DUF580; 1.
SQ SEQUENCE 651 AA; 72937 MW; A26613B3055420AF CRC64;

Query Match 4.0%; Score 18; DB 2; Length 651;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 SEFILACQOMTIAGAVVT 200
DB 392 SEFILACQOMTIAGAVVT 409
|||||
RESULT 7
Q6IR74 XENLA
ID Q6IR74_XENLA PRELIMINARY; PRT; 651 AA.
AC Q6IR74;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE MGC82240 protein.
GN Name=MGC82240;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
[1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Rouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strauberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus

RT initiative";
RL Dev. Dyn. 225:384-391(2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Klein S., Strauberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
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CC
CC
DR EMBL; BC071026; AAH71026.1; -; mRNA.
DR InterPro; IPR007603; DUF580.
DR PANTHER; PTHR12385; DUF580; 1.
DR Pfam; PF04515; DUF580; 1.
SQ SEQUENCE 651 AA; 72908 MW; 619A2CB2C848FOAF CRC64;

Query Match 4.0%; Score 18; DB 2; Length 651;
Best Local Similarity 100.0%; Pred. No. 6.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 SEFILACQOMTIAGAVVT 200
DB 392 SEFILACQOMTIAGAVVT 409
|||||
RESULT 8
Q4T3N9 TETNG
ID Q4T3N9_TETNG PRELIMINARY; PRT; 94 AA.
AC Q4T3N9;
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Chromosome undetermined SCAF9971, whole genome shotgun sequence.
DE (Fragments).
GN ORFNames=GSTENG0000709001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontoidea; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
[1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jallion O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segreus B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Landt V., Schacher V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RL the early vertebrate proto-karyotype";
RL Nature 431:946-957(2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RP Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
RL - CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
CC
DR EMBL; CAAEI0009971; CAF92493.1; -; Genomic_DNA.
DR InterPro; IPR007603; DUF580.

DR PANTHER; PTHR12385; DUF580; 1.
 FT NON TER 1 1
 SQ SEQUENCE 94 AA; 10954 MW; D9C6AAEF02ED9824 CRC64;
 Query Match 2.5%; Score 11; DB 2; Length 94;
 Best Local Similarity 100.0%; Pred. No. 0.085;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 190 QQMTIAGAVT 200
 Db 59 QQMTIAGAVT 69
 RESULT 9
 CTL1_MOUSE STANDARD; PRT; 653 AA.
 AC Q6X893; Q6X894; Q8R0Y4; Q91229;
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 30-AUG-2005, sequence version 2.
 DT 07-MAR-2006, entry version 15.
 DE Choline transporter-like protein 1 (Solute carrier family 44 member 1)
 DE (CD92 antigen) (CDW92).
 GN Name=Slc44a1; Synonyms=Cdw92, Ctl1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), TISSUE SPECIFICITY,
 RP SUBCELLULAR LOCATION, AND FUNCTION.
 RC TISSUE=Fibroblast;
 RX PubMed=15474312; DOI=10.1016/j.gene.2004.07.042;
 RA Yuan Z., Wagner L., Poloumienko A., Bakovic M.;
 RT "Identification and expression of a mouse muscle-specific CTL1 gene."
 RL Gene 341:305-312 (2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 390-653 (ISOFORM 1).
 RC STRAIN=FVB/N; TISSUE=Liver, and Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausberg R.L., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Probable choline transporter. May be involved in
 CC membrane synthesis and myelin production.
 CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=A;
 CC IsoId=Q6X893-1; Sequence=Displayed;
 CC Name=2; Synonyms=B;
 CC IsoId=Q6X893-2; Sequence=VSP_015428;
 CC -1- TISSUE SPECIFICITY: Specifically abundant in skeletal muscle (at
 CC protein level).
 CC -1- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
 CC -----

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 CC -----
 DR EMBL; AY249865; AAP81042.1; -; mRNA.
 DR EMBL; AY249866; AAP81043.1; -; mRNA.
 DR EMBL; BC010258; AAH10258.1; -; mRNA.
 DR EMBL; BC025941; AAH25941.1; ALT INIT; mRNA.
 DR Ensembl; ENSMUSG0000028412; Mus musculus.
 DR MGI; MGI:2140592; Slc44a1.
 DR GO; GO:0016021; C:integral to membrane; IDA.
 DR GO; GO:0015220; F:choline transporter activity; IDA.
 DR GO; GO:0015871; P:choline transport; IDA.
 DR InterPro; IPR007603; DUF580.
 DR Pfam; PF04515; DUF580; 1.
 KW Alternative splicing; Membrane; Transmembrane; Transport.
 FT CHAIN 1 653 Choline transporter-like protein 1.
 FT /FTID=PRO_0000191713.
 FT Cytoplasmic (Potential).
 FT Extracellular (Potential).
 FT Potential.
 FT TOPO_DOM 1 29
 FT TRANSMEM 30 50
 FT TOPO_DOM 51 211
 FT TRANSMEM 212 232
 FT TOPO_DOM 233 237
 FT TRANSMEM 238 258
 FT TOPO_DOM 259 287
 FT TRANSMEM 288 308
 FT TOPO_DOM 309 314
 FT TRANSMEM 315 335
 FT TOPO_DOM 336 337
 FT TRANSMEM 338 358
 FT TOPO_DOM 359 379
 FT TRANSMEM 380 400
 FT TOPO_DOM 401 441
 FT TRANSMEM 442 462
 FT TOPO_DOM 463 536
 FT TRANSMEM 537 557
 FT TOPO_DOM 558 565
 FT TRANSMEM 566 586
 FT TOPO_DOM 587 653
 FT COMPBIAS 473 491
 FT VARSPPLIC 650 653
 FT LRRK -> VGSBEAAALHDFPHFVSVCVFTDCTSSGEAL
 VVCITQDMLLFACLPITWMAEVLSQLRPLSVKVS (in
 isoform 2).
 FT /FTID=VSP_015428.
 FT L -> P (in Ref. 2; AAH25941).
 FT F -> L (in Ref. 2; AAH25941).
 FT L -> F (in Ref. 2; AAH25941).
 SQ SEQUENCE 653 AA; 73083 MW; 3857DA8BE428EFF5 CRC64;
 Query Match 2.5%; Score 11; DB 1; Length 653;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 183 SEFILACQOMT 193
 Db 395 SEFILACQOMT 405
 RESULT 10
 CTL1_MOUSE STANDARD; PRT; 656 AA.
 AC Q8V1I6; Q9JUZ7;
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 01-MAR-2002, sequence version 1.
 DT 07-MAR-2006, entry version 21.
 DE Choline transporter-like protein 1 (Solute carrier family 44 member 1)
 DE (CD92 antigen) (CDW92).
 GN Name=Slc44a1; Synonyms=Cdw92, Ctl1;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=20144127; PubMed=10677542; DOI=10.1073/pnas.030339697;
RA O'Regan S., Traiffort E., Ruat M., Cha N., Compaore D., Meunier F.-M.;
RT "An electric lobe suppressor for a yeast choline transporter mutation
RT belongs to a new family of transporter-like proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1835-1840(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1), FUNCTION, AND TISSUE
RP SPECIFICITY.
RC STRAIN=Wistar; TISSUE=Brain;
RX PubMed=15715662; DOI=10.1111/j.1471-4159.2004.02962.x;
RA Traiffort E., Ruat M., O'Regan S., Meunier F.-M.;
RT "Molecular characterization of the family of choline transporter-like
RT proteins and their splice variants.";
RL J. Neurochem. 92:1116-1125(2005).
RN [3]
RP INDUCTION.
RX PubMed=12007839; DOI=10.1016/S0169-328X(02)00182-1;
RA Che Y.H., Yamashita T., Higuchi H., Toyama M.;
RT "Changes in mRNA for choline transporter-like protein following facial
RT nerve transection.";
RL Brain Res. Mol. Brain Res. 101:122-125(2002).
RN [4]
RP FUNCTION, AND TISSUE SPECIFICITY.
RX PubMed=16000150; DOI=10.1111/j.1471-4159.2005.03299.x;
RA Inazu M., Takeda H., Matsumiya T.;
RT "Molecular and functional characterization of an Na-independent
RT choline transporter in rat astrocytes.";
RL J. Neurochem. 94:1427-1437(2005).
RN [5]
RP INDUCTION.
RX PubMed=15691711; DOI=10.1016/j.mcn.2004.09.014;
RA Leconte M.-J., De Gois S., Guerci A., Ravassard P., Faucon Biguet N.,
RA Mallet J., Berrard S.;
RT "Differential expression and regulation of the high-affinity choline
RT transporter CHTL and choline acetyltransferase in neurons of superior
RT cervical ganglia.";
RL Mol. Cell. Neurosci. 28:303-313(2005).
CC -1- FUNCTION: Probable choline transporter. May be involved in
CC membrane synthesis and myelin production.
CC -1- INDUCTION: By leukemia inhibitory factor or retinoic acid in
CC vitro. In vivo, induced during the axonal elongation period
CC following axotomy.
CC -1- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
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CC -----
CC EMBL; AJ245619; CAB75555.1; -; mRNA.
CC EMBL; AJ245619; CAB75555.1; -; mRNA.
CC Ensembl; ENSRNOG0000017846; Rattus norvegicus.
CC RGD; 621426; Cdw92.
CC InterPro; IPR007603; DUF580.
CC PANTHER; PTHR12385; DUF580; 1.
CC Pfam; PF04515; DUF580; 1.
CC Alternative splicing; Membrane; Transmembrane; Transport.
KW CHAIN 1 656 Choline transporter-like protein 1.
FT FTId=PRO_0000191714.
FT TOPO_DOM 1 29 Cytoplasmic (Potential).
FT TRANSMEM 30 50 Potential.
FT TOPO_DOM 51 211 Extracellular (Potential).
FT TRANSMEM 212 232 Potential.

FT TOPO_DOM 233 237 Cytoplasmic (Potential).
FT TRANSMEM 238 258 Potential.
FT TOPO_DOM 259 287 Extracellular (Potential).
FT TRANSMEM 288 308 Potential.
FT TOPO_DOM 309 314 Cytoplasmic (Potential).
FT TRANSMEM 315 335 Potential.
FT TOPO_DOM 336 337 Extracellular (Potential).
FT TRANSMEM 338 358 Potential.
FT TOPO_DOM 359 379 Cytoplasmic (Potential).
FT TRANSMEM 380 400 Potential.
FT TOPO_DOM 401 441 Extracellular (Potential).
FT TRANSMEM 442 462 Potential.
FT TOPO_DOM 463 536 Cytoplasmic (Potential).
FT TRANSMEM 537 557 Potential.
FT TOPO_DOM 558 565 Extracellular (Potential).
FT TRANSMEM 566 586 Potential.
FT TOPO_DOM 587 656 Cytoplasmic (Potential).
FT COMPTIAS 473 491 Cys-rich.
FT VARSPPLIC 650 653 ASGA -> LRKR (in isoform 2).
FT VARSPPLIC 654 656 /FTId=VSP_015429.
FT Missing (in isoform 2).
FT CONFLICT 267 267 /FTId=VSP_015430.
FT CONFLICT 645 645 R -> S (in Ref. 1).
FT CONFLICT 645 645 K -> E (in Ref. 1).
SQ SEQUENCE 656 AA; 73092 MW; 217RAD02F6B4D138 CRC64;
Query Match 2.5%; Score 11; DB 1; Length 656;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 183 SEFILACQMT 193
DB 395 SEFILACQMT 405
|||||
|||
RESULT 11
CTLI_HUMAN STANDARD; PRT; 657 AA.
ID CTLI_HUMAN Q8WV03; Q8WV03; Q96K03; Q9NY69;
AC Q8WV03; Q8WV03; Q8WV03; Q8WV03; Q8WV03;
DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2002, sequence version 1.
DT 07-MAR-2006, entry version 27.
DE Choline transporter-like protein 1 (Solute carrier family 44 member 1
DE (CD92 antigen) (CDW92).
DE Name=SLC44A1; Synonyms=CDW92, CTL1;
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OC NCBI_TaxID=9606;
OX [1]
RN NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND ALTERNATIVE SPLICING (ISOFORM
RP 2).
RC TISSUE=Ewing sarcoma;
RX MEDLINE=20144127; PubMed=10677542; DOI=10.1073/pnas.030339697;
RA O'Regan S., Traiffort E., Ruat M., Cha N., Compaore D., Meunier F.-M.;
RT "An electric lobe suppressor for a yeast choline transporter mutation
RT belongs to a new family of transporter-like proteins.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1835-1840(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 3), AND TISSUE SPECIFICITY.
RX MEDLINE=21555187; PubMed=11698453;
RA Wille S., Szekeres A., Majdic O., Prager E., Staffler G., Stoeckl J.,
RA Kunthaler D., Prieschl E.E., Baumrucker T., Bartscher H.,
RA Zlabinger G.J., Knapp W., Stockinger H.;
RT "Characterization of CDw92 as a member of the choline transporter-like
RT protein family regulated specifically on dendritic cells.";
RL J. Immunol. 167:5795-5804(2001).
RN [3]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
RC TISSUE=Ewing sarcoma;
RX PubMed=15715662; DOI=10.1111/j.1471-4159.2004.02962.x;
RA Traiffort E., Ruat M., O'Regan S., Meunier F.-M.;

RT "Molecular characterization of the family of choline transporter-like
 RT proteins and their splice variants.";
 RL J. Neurochem. 92:1116-1125 (2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RA PubMed=15164053; DOI=10.1038/nature02465;
 RA Humphray S.J., Oliver K., Hunt A.R., Plumb R.W., Loveland J.E.,
 RA Ainscough R., Almeida J.P., Ambrose K.D., Searle S., Hunt S.E., Scott C.E., Jones M.C.,
 RA Babbage A.K., Babbage S., Bagnuley C.L., Bailey J., Banerjee R.,
 RA Barker D.J., Barlow K.F., Bates K., Beasley H., Beasley O., Bird C.P.,
 RA Bray-Allen S., Brown A.J., Brown J.Y., Burford D., Burrill W.,
 RA Burton J., Carder C., Carter N.P., Chapman J.C., Chen Y., Clarke G.,
 RA Clark S.Y., Clee C.M., Clegg S., Collier R.E., Corby N., Crosier M.,
 RA Cummings A.T., Davies J., Dhali P., Dunn M., Dutta I., Dyer L.W.,
 RA Earthrowl M.E., Faulkner L., Fleming C.J., Frankish A.,
 RA Frankland J.A., French L., Fricker D.G., Garner P., Garnett J.,
 RA Ghori J., Gilbert J.G.R., Glison C., Grafham D.V., Gribble S.,
 RA Griffiths C., Griffiths-Jones S., Grocock R., Guy J., Hall R.E.,
 RA Hammond S., Harley J.L., Harrison E.S.I., Hart E.A., Heath P.D.,
 RA Henderson C.D., Hopkins B.L., Howard P.J., Howden P.J., Huckle E.,
 RA Johnson C., Johnson D., Joy A.A., Kay M., Keenan S., Kershaw J.K.,
 RA Kimberley A.M., King A., Knights A., Laird G.K., Langford C.,
 RA Lawlor S., Leongamornlert D.A., Leversha M., Lloyd C., Lloyd D.M.,
 RA Lovell J., Martin S., Maehregchi-Mohammadi M., Matthews L., McLaren S.,
 RA McIay K.E., McMurray A., Milne S., Nickerson T., Nisbett J.,
 RA Nordieck G., Pearce A.V., Peck A.I., Porter K.M., Pandian R.,
 RA Pellan S., Phillimore B., Povey S., Ramsey Y., Rand V., Scharfe M.,
 RA Sehra H.K., Showkneen R., Sims S.K., Skuce C.D., Smith M.,
 RA Steward C.A., Swarbreck D., Sycamore N., Tester J., Thorpe A.,
 RA Tracey A., Tromans A., Thomas D.W., Wall M., Wallis J.M., West A.P.,
 RA Whitehead S.L., Willey D.B., Williams S.A., Wilming L., Wray P.W.,
 RA Young L., Ashurst J.L., Coulson A., Blocker H., Durbin R.,
 RA Sulston J.E., Hubbard T., Jackson M.J., Bentley D.R., Beck S.,
 RA Rogers J., Dunham I.;
 RT "DNA sequence and analysis of human chromosome 9";
 RL Nature 429:369-374 (2004).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RA TISSUE=Eye, and Lung;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Harte S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 CC -1- FUNCTION: Probable choline transporter. May be involved in
 CC membrane synthesis and myelin production (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
 CC similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=A;
 CC IsoId=Q8WWI5-1; Sequence=Displayed;
 CC Name=2; Synonyms=B;
 CC IsoId=Q8WWI5-2; Sequence=VSP_015424, VSP_015425;
 CC Name=3; Synonyms=C;
 CC IsoId=Q8WWI5-3; Sequence=VSP_015426, VSP_015427;

CC -1- TISSUE SPECIFICITY: Expressed in various cells of the
 CC hematopoietic system.
 CC -1- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
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 CC -----
 CC ENBL; AJ245620; CAB75541.2; -; Genomic_DNA.
 DR ENBL; AJ273365; CAC82175.1; -; mRNA.
 DR ENBL; AJ420812; CAD12764.1; -; Genomic_DNA.
 DR ENBL; AL161627; CAI13069.1; -; Genomic_DNA.
 DR ENBL; AL450265; CAI13069.1; JOINED; Genomic_DNA.
 DR ENBL; AL590368; CAI13069.1; JOINED; Genomic_DNA.
 DR ENBL; AL161627; CAI13070.1; -; Genomic_DNA.
 DR ENBL; AL450265; CAI13070.1; JOINED; Genomic_DNA.
 DR ENBL; AL590368; CAI13070.1; JOINED; Genomic_DNA.
 DR ENBL; AL161627; CAI13071.1; -; Genomic_DNA.
 DR ENBL; AL590368; CAI13071.1; JOINED; Genomic_DNA.
 DR ENBL; AL590368; CAI13071.1; JOINED; Genomic_DNA.
 DR ENBL; AL450265; CAI14395.1; -; Genomic_DNA.
 DR ENBL; AL161627; CAI14395.1; JOINED; Genomic_DNA.
 DR ENBL; AL590368; CAI14395.1; JOINED; Genomic_DNA.
 DR ENBL; AL450265; CAI14395.1; JOINED; Genomic_DNA.
 DR ENBL; AL161627; CAI14396.1; -; Genomic_DNA.
 DR ENBL; AL590368; CAI14396.1; JOINED; Genomic_DNA.
 DR ENBL; AL450265; CAI14397.1; -; Genomic_DNA.
 DR ENBL; AL161627; CAI14397.1; JOINED; Genomic_DNA.
 DR ENBL; AL590368; CAI14397.1; JOINED; Genomic_DNA.
 DR ENBL; AL590368; CAH73434.1; -; Genomic_DNA.
 DR ENBL; AL161627; CAH73434.1; JOINED; Genomic_DNA.
 DR ENBL; AL450265; CAH73434.1; JOINED; Genomic_DNA.
 DR ENBL; AL590368; CAH73435.1; -; Genomic_DNA.
 DR ENBL; AL161627; CAH73435.1; JOINED; Genomic_DNA.
 DR ENBL; AL590368; CAH73436.1; -; Genomic_DNA.
 DR ENBL; AL161627; CAH73436.1; JOINED; Genomic_DNA.
 DR ENBL; EC018213; AAH18213.1; -; mRNA.
 DR ENBL; EC049203; AAH49203.1; -; mRNA.
 DR Ensembl; ENSG00000070214; Homo sapiens.
 DR HGNC; HGNC:18798; SLC44A1.
 DR MIM; 606105; gene.
 DR InterPro; IPR007603; DUF580.
 DR PANTHER; PTHR12385; DUF580; 1.
 DR Pfam; PF04515; DUF580; 1.
 KW Alternative splicing; Antigen; Membrane; Transmembrane; Transport.
 FT CHAIN 1 657 Choline transporter-like protein 1.
 FT TOPO_DOM 1 30 /FTid=PRO_000019172.
 FT TRANSMEM 31 51 Cytoplasmic (Potential).
 FT TOPO_DOM 52 212 Extracellular (Potential).
 FT TRANSMEM 213 233 Potential.
 FT TOPO_DOM 234 238 Cytoplasmic (Potential).
 FT TRANSMEM 239 259 Potential.
 FT TOPO_DOM 260 288 Extracellular (Potential).
 FT TRANSMEM 289 309 Potential.
 FT TOPO_DOM 310 335 Cytoplasmic (Potential).
 FT TRANSMEM 316 336 Potential.
 FT TOPO_DOM 337 338 Extracellular (Potential).
 FT TRANSMEM 339 359 Potential.
 FT TOPO_DOM 360 380 Cytoplasmic (Potential).
 FT TRANSMEM 381 401 Potential.
 FT TOPO_DOM 402 442 Extracellular (Potential).
 FT TRANSMEM 443 463 Potential.
 FT TOPO_DOM 464 537 Cytoplasmic (Potential).
 FT TRANSMEM 538 558 Extracellular (Potential).
 FT TOPO_DOM 559 566 Potential.
 FT TRANSMEM 567 587 Potential.
 FT TOPO_DOM 588 657 Cytoplasmic (Potential).
 FT COMPBias 474 492 ASGA -> LKXR (in isoform 2).
 FT VARSPlic 651 654 /FTid=VSP_015424.
 FT VARSPlic 651 652 AS -> IK (in isoform 3).

```
FT VARSPLIC 653 657 /FTid=VSP_015426.
FT Missing (in isoform 3).
FT /FTid=VSP_015427.
FT VARSPLIC 655 657 Missing (in isoform 2).
FT /FTid=VSP_015425.
FT CONFLICT 79 79 I -> V (in Ref. 2).
FT CONFLICT 644 644 S -> A (in Ref. 2).
SQ SEQUENCE 657 AA; 73302 MW; 10D70CAB8E33E3AC CRC64;

Query Match 2.5%; Score 11; DB 1; Length 657;
Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 183 SEFILACQOMT 193
Db 396 SEFILACQOMT 406

RESULT 12
Q7QSR7_ANOGA PRELIMINARY; PRT; 677 AA.
AC Q7QSR7;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 2.
DT 07-FEB-2006, entry version 10.
DE ENSANGP0000020538 (Fragment).
GN ORFNAMES=ENSANGG0000018049;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; AAAB01008960; EAA10766.2; -; Genomic_DNA.
DR InterPro; IPR007603; DUF580.
DR PANTHER; PTHR12385; DUF580; 1.
DR Pfam; PF04515; DUF580; 1.
DR NON_TER 677 677
SQ SEQUENCE 677 AA; 76258 MW; 0EB24759D946739E CRC64;

Query Match 2.2%; Score 10; DB 2; Length 677;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 177 IGLIWTSEFI 186
Db 418 IGLIWTSEFI 427

RESULT 13
Q4H957_9DEIO PRELIMINARY; PRT; 155 AA.
AC Q4H957;
DT 16-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 16-AUG-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DT
```

```
DE Hypothetical protein precursor.
GN ORFNAMES=Dgeodraft_1048;
OS Deinococcus geothermalis DSM 11300.
OC Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=319795;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 11300;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Deinococcus geothermalis
RT DSM 11300.";
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DSM 11300;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Deinococcus geothermalis
RT DSM 11300.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
DR EMBL; AAHE01000005; EAL82795.1; -; Genomic_DNA.
DR Hypothetical protein; Signal.
FT SIGNAL 1 35 Potential.
SQ SEQUENCE 155 AA; 16438 MW; 535B68D3C554DC35 CRC64;

Query Match 2.0%; Score 9; DB 2; Length 155;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 LWVAVLLSL 146
Db 18 LWVAVLLSL 26

RESULT 14
Q9A2U8_CAUCR PRELIMINARY; PRT; 263 AA.
AC Q9A2U8;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein CC3458.
GN OrderedLocusNames=CC3458;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Smolovaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,
RA Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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CC -----
DR EMBL; AE006004; AAK25420.1; -; Genomic_DNA.
DR PIR; H87677; H87677.
DR TIGR; CC3458; -.
DR InterPro; IPR003675; Abi.
DR Pfam; PF02517; Abi; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 263 AA; 28189 MW; 1AFB12DDA9E9E1D8 CRC64;

Query Match      2.0%; Score 9; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LALALSLAM 21
Db 95 LALALSLAM 103

RESULT 15
Q74K77_LACJO
ID Q74K77_LACJO PRELIMINARY; PRT; 77 AA.
AC Q74K77;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Hypothetical protein.
GN OrderedLocusNames=LJ0876; ORFNames=LJ_0876;
OS Lactobacillus johnsonii.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=33959;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=NCC 533;
RA PubMed=14983040; DOI=10.1073/pnas.0307327101;
RA Priddy R.D., Berger B., Desiere F., Vilanova D., Barretto C.,
RA Pittet A.-C., Zwaalen M.-C., Rouvet M., Altermann E., Barrangou R.,
RA Mollet B., Mercenier A., Kleenhammer T., Arigoni F., Schell M.A.;
RT "The genome sequence of the probiotic intestinal bacterium
RT Lactobacillus johnsonii NCC 533."
RL Proc. Natl. Acad. Sci. U.S.A. 101:2512-2517(2004).
CC -----
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CC -----
DR EMBL; AE017198; AAS08697.1; -; Genomic_DNA.
DR BioCyc; LJOH257314:LJ0876-MONOMER; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0015450; F:protein translocase activity; IEA.
DR GO; GO:0009306; P:protein secretion; IEA.
DR InterPro; IPR004692; SecG.
DR Pfam; PF03840; SecG; 1.
DR PRINTS; PR01651; SECSEXPORT.
DR TIGRFAMs; TIGR00810; secg; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 77 AA; 8398 MW; C64B75955SA84D18 CRC64;

Query Match      1.8%; Score 8; DB 2; Length 77;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 ITAVLLVL 93
Db 56 ITAVLLVL 63

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Search completed: June 6, 2006, 22:29:22
Job time : 299 secs

GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 6, 2006, 22:24:36 ; Search time 41 Seconds
(without alignments)
1044.304 Million cell updates/sec

Title: US-10-063-537-32
Perfect score: 445
Sequence: 1 MSGRDTILGLTILALSLA.....QQDKSLRNEEGTELOAIVR 445

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 6
Total number of hits satisfying chosen parameters: 2646

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	2.0	263	2 H87677	conserved hypother
2	8	1.8	132	2 D82670	general secretory
3	8	1.8	268	2 A64123	cryptophan synthas
4	8	1.8	293	2 B83783	hypothetical prote
5	8	1.8	293	2 T27430	hypothetical prote
6	8	1.8	360	2 I53032	bone morphogenetic
7	8	1.8	472	1 BMHU3	bone morphogenetic
8	8	1.8	761	2 S66719	hypothetical prote
9	8	1.8	764	2 T43751	cytochrome-c oxida
10	8	1.8	962	2 D70661	probable membranep
11	8	1.8	1023	2 AE1280	ATP-dependent dsDN
12	8	1.8	1023	2 AE1643	ATP-dependent dsDN
13	8	1.8	1578	2 S76238	hypothetical prote
14	7	1.6	48	2 B64647	hypothetical prote
15	7	1.6	51	2 D81271	small hydrophobic
16	7	1.6	52	2 AD1716	hypothetical prote
17	7	1.6	89	2 A69833	hypothetical prote
18	7	1.6	93	2 S66290	alpha 1 antichymot
19	7	1.6	98	2 E90606	hypothetical prote
20	7	1.6	112	2 S75298	hypothetical prote
21	7	1.6	112	2 AE2244	hypothetical prote
22	7	1.6	143	2 C84118	hypothetical prote
23	7	1.6	146	2 H75394	conserved hypother
24	7	1.6	161	2 S04765	LAT52 protein prec
25	7	1.6	165	2 G72486	hypothetical prote
26	7	1.6	166	2 S60634	cytochrome-c oxida
27	7	1.6	166	2 S25600	cytochrome-c oxida
28	7	1.6	166	2 G75478	ribosomal protein
29	7	1.6	181	2 AH3518	hypothetical prote

30	7	1.6	185	2 D82828	dTDP-4-dehydroxam
31	7	1.6	185	2 G89895	conserved hypother
32	7	1.6	199	2 T26157	hypothetical prote
33	7	1.6	199	2 T19616	hypothetical prote
34	7	1.6	207	2 F64223	hypothetical prote
35	7	1.6	207	2 B75327	hypothetical prote
36	7	1.6	209	2 A90608	hypothetical prote
37	7	1.6	210	2 G72507	hypothetical prote
38	7	1.6	212	2 T12644	NADH2 dehydrogenas
39	7	1.6	215	2 E70102	S-adenosylmethioni
40	7	1.6	223	2 T35424	probable regulator
41	7	1.6	226	2 H83185	hypothetical prote
42	7	1.6	234	2 H98154	amino acid ABC tra
43	7	1.6	234	2 AD3133	hypothetical prote
44	7	1.6	247	2 AD0757	cobalamin (5'-phos
45	7	1.6	248	2 C90984	probable glycosyl

ALIGNMENTS

RESULT 1

H87677 conserved hypothetical protein CC3458 [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: H87677

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonchak, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: H87677

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-263 <STO>

A;Cross-references: UNIPROT:Q9A2U8; UNIPARC:UPI000000C7AAB; GB:AE003673; NID:gl3425176; PJ

C;Genetics:

A;Gene: CC3458

Query Match 2.0%; Score 9; DB 2; Length 263;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	13	LALALS	21
DB	95	LALALS	103

RESULT 2

D82670

general secretory pathway protein I precursor XF1521 [imported] - Xylella fastidiosa (str)

C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C;Accession: D82670

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: D82670

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-132 <SIM>

A;Cross-references: UNIPROT:Q9PD58; UNIPARC:UPI000000C2760; GB:AE003849; NID

A;Experimental source: strain 9asc

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, P.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigret

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, B.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
M.; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv
M.; Tuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1521
C;Superfamily: general secretion pathway protein I precursor

Query Match 1.8%; Score 8; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 ILALALS 19
Db 18 ILALALS 25

RESULT 3
A64123
tryptophan synthase (EC 4.2.1.20) alpha chain - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: A64123
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: A64123
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-268 <TIGR>
A;Cross-references: UNIPROT:P43759; UNIPARC:UPI00001374CE; GB:U32822; GB:I42023; NID:gl5
C;Genetics:
A;Gene: trpA
C;Function:
A;Description: catalyzes conversion of indoleglycerol phosphate and serine to tryptophan
A;Pathway: tryptophan biosynthesis
A;Note: cofactor pyridoxal phosphate
C;Superfamily: tryptophan synthase alpha chain; tryptophan synthase alpha chain homology
C;Keywords: carbon-oxygen lyase; hydro-lyase; tryptophan biosynthesis
F;18-247/Domain: tryptophan synthase alpha chain homology <TRPA>
F;49/Active site: Glu #status: predicted

Query Match 1.8%; Score 8; DB 2; Length 268;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 144 LSLGTAGA 151
Db 225 LSLGTAGA 232

RESULT 4
B83783
hypothetical protein BH1066 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: B83783
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83783
A;Status: preliminary
A;Molecule type: DNA

Query Match 1.8%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SLSILFF 224
Db 331 SLSILFF 338

RESULT 7
BMH03

A;Residues: 1-293 <STO>
A;Cross-references: UNIPROT:O9KD25; UNIPARC:UPI00000C3AA3; GB:AP001510; GB:BA000004; NID:
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1066
C;Superfamily: maltose transport protein malG

Query Match 1.8%; Score 8; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 234 SFLISVVR 241
Db 74 SFLISVVR 81

RESULT 5
T27430
hypothetical protein Y79H2A.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27430
R;Matthews, L.
submitted to the EMBL Data Library, September 1999
A;Reference number: Z20365
A;Accession: T27430
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-293 <WIL>
A;Cross-references: UNIPROT:O9UIR9; UNIPARC:UPI000061335; EMBL:AL110501; NID:e1542357; I
A;Experimental source: clone Y79H2A
C;Genetics:
A;Gene: CESP.Y79H2A.2
A;Introns: 30/3; 50/1; 85/1; 112/3; 180/3; 223/3
C;Superfamily: Caenorhabditis elegans hypothetical protein Y79H2A.2

Query Match 1.8%; Score 8; DB 2; Length 293;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 IFISLVIL 42
Db 23 IFISLVIL 30

RESULT 6
I53032
bone morphogenetic protein 3 - rat (fragment)
C;Species: Rattus sp. (rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C;Accession: I53032
R;Chen, D.; Feng, J.Q.; Feng, M.; Harris, M.A.; Mahy, P.; Mundy, G.R.; Harris, S.E.
DNA Cell Biol. 14, 235-239, 1995
A;Title: Sequence and expression of bone morphogenetic protein 3 mRNA in prolonged cultu
A;Reference number: I53032; MUID:95186061; PMID:7880444
A;Accession: I53032
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-360 <RES>
A;Cross-references: UNIPARC:UPI0000170CBA; GB:S77492; NID:g957225; PIDN:AAB33725.1; PID:g
C;Superfamily: inhibin

Query Match 1.8%; Score 8; DB 2; Length 360;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SLSILFF 224
Db 331 SLSILFF 338

RESULT 7
BMH03

bone morphogenetic protein 3 precursor - human
N;Alternate names: osteogenin
C;Species: Homo sapiens (man)
C;Date: 16-Sep-1992 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: D37278
R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz, R.W.; Hew
Science 242, 1528-1534, 1988
A;Title: Novel regulators of bone formation: molecular clones and activities.
A;Reference number: A37278; MUID:89072730; PMID:3201241
A;Accession: D37278
A;Molecule type: mRNA
A;Residues: 1-472 <W04>
A;Cross-references: UNIPROT:P12645; UNIPARC:UPI0000126A25; GB:M22491; NID:g179505; PIDN:
C;Genetics:
A;Gene: GDB:BMP3
A;Cross-references: GDB:125206; OMIM:112263
A;Map position: 4p14-4q21
C;Superfamily: inhibin
C;Keywords: bone; glycoprotein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-345/Domain: propeptide #status predicted <PRO>
F;346-472/Product: bone morphogenetic protein 3 #status predicted <MAT>
F;117,141,175,220,463/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 1.8%; Score 8; DB 1; Length 472;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 SSLSILFF 224
Db 443 SSLSILFF 450
|||||

RESULT 8
S66719
hypothetical protein YOL036w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2105
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C;Accession: S66719
R;Habbig, B.; Hattenhorst, U.; Hollenbergh, C.P.; Ramezani Rad, M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66703
A;Accession: S66719
A;Molecule type: DNA
A;Residues: 1-761 <HAB>
A;Cross-references: UNIPROT:Q08206; UNIPARC:UPI000006C3BA; EMBL:Z74779; NID:g1419828; PI
A;Experimental source: strain S288C
C;Genetics:
A;Gene: MIPS:YOL036w
A;Cross-references: SGD:S0005396
A;Map position: 15L

Query Match 1.8%; Score 8; DB 2; Length 761;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 308 KILSKNSS 315
Db 624 KILSKNSS 631
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RESULT 9
T43751
cytochrome-c oxidase (EC 1.9.3.1) chain 1/2 [similarity] - slime mold (Dictyostelium dis
C;Species: mitochondrion Dictyostelium discoideum
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43751
R;Ogawa, S.; Yoshino, R.; Angata, K.; Pi, M.; Iwamoto, M.; Kuroe, K.; Matsuo, K.; Morio,
submitted to the EMBL Data Library, December 1996
A;Description: The mitochondrial DNA of Dictyostelium discoideum. Complete sequence, gen
A;Reference number: Z22666
A;Accession: T43751

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-764 <OGA>
A;Cross-references: UNIPROT:O21042; UNIPARC:UPI0000090BE1; EMBL:AB000109; PIDN:BAA78055.1
C;Genetics:
A;Gene: cox1/2
A;Genome: mitochondrion
A;Introns: 89/2; 258/3; 387/3; 637/3
C;Superfamily: Acanthamoeba cytochrome-c oxidase chain I/II; cytochrome-c oxidase chain
C;Keywords: copper; electron transfer; heme; iron; magnesium; membrane-associated complex
F;80,396/Binding site: heme a iron (His) (axial ligands) #status predicted
F;259,308,309/Binding site: copper (His) #status predicted
F;259-263/Cross-link: 1'-histidyl-3'-tyrosine (His-Tyr) #status predicted
F;263/Binding site: oxygen (Tyr) #status predicted
F;386,736/Binding site: magnesium (His, Glu) #status predicted
F;394/Binding site: heme a3 iron (His) (axial ligand) #status predicted
F;699,734,738,745/Binding site: copper 1 (His, Cys, Met) #status predicted
F;734,736,738,742/Binding site: copper 2 (Cys, Glu, Cys, His) #status predicted

Query Match 1.8%; Score 8; DB 2; Length 764;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 ITAVLLVL 93
Db 209 ITAVLLVL 216
|||||

RESULT 10
D70661
probable membraneprotein with strong - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: D70661
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70661
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-962 <COL>
A;Cross-references: UNIPROT:P95235; UNIPARC:UPI000012F275; GB:Z83860; GB:AL123456; NID:g-
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: mmpL9

Query Match 1.8%; Score 8; DB 2; Length 962;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 VLLSLGTA 149
Db 802 VLLSLGTA 809
|||||

RESULT 11
AE1280
ATP-dependent dsDNA exonuclease SbcC homolog lmo1645 [imported] - Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE1280
R;Glaser, P.; Frangul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AE1280
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1023 <GLA>
A;Cross-references: UNIPROT:Q9Y6N9; UNIPARC:UPI000005500D; GB:NC_003210; PIDN:CAC99723.1
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1645

Query Match 1.8%; Score 8; DB 2; Length 1023;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LALALSIA 20
Db 935 LALALSIA 942
|||||

RESULT 12
AE1643
ATP-dependent dsDNA exonuclease SbcC homolog sbcC [imported] - *Listeria innocua* (strain
C;Species: *Listeria innocua*
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE1643
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Katst, U.
Science 294, 849-852, 2001
A;Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournan, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant,
A;Title: Comparative Genomics of *Listeria* species.
A;Reference number: AB1077; MUID:2157279; PMID:11679669
A;Accession: AE1643
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1023 <GLA>
A;Cross-references: UNIPROT:Q92B64; UNIPARC:UPI000000CC623; GB:AL592022; PIDN:CAC96917.1;
A;Experimental source: strain Clp11262
C;Genetics:
A;Gene: sbcC

Query Match 1.8%; Score 8; DB 2; Length 1023;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LALALSIA 20
Db 935 LALALSIA 942
|||||

RESULT 13
S76238
hypothetical protein sil0267 - *Synechocystis* sp. (strain PCC 6803)
C;Species: *Synechocystis* sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S76238
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S76238
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1578 <KAN>
A;Cross-references: UNIPROT:P74400; UNIPARC:UPI00000C10E9; EMBL:D90914; GB:AB001339; NID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 1.8%; Score 8; DB 2; Length 1578;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 AVLLVLIIF 95
Db 23 AVLLVLIIF 30
|||||

RESULT 14

B64647
hypothetical protein HP1018 - *Helicobacter pylori* (strain 26695)
C;Species: *Helicobacter pylori*
C;Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C;Accession: B64647
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.;
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.N
A;Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.
A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: B64647
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-48 <TOM>
A;Cross-references: UNIPROT:Q25662; UNIPARC:UPI00000C08DD; GB:AE000610; GB:AE000511; NID:

Query Match 1.6%; Score 7; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 LALALS 19
Db 9 LALALS 15
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RESULT 15

D81271
small hydrophobic protein Cj1728c [imported] - *Campylobacter jejuni* (strain NCTC 11168)
C;Species: *Campylobacter jejuni*
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: D81271
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrell
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen *Campylobacter jejuni* reveals hyp
A;Reference number: AB1250; MUID:20150912; PMID:10688204
A;Accession: D81271
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-51 <PAR>
A;Cross-references: UNIPROT:Q9PLV0; UNIPARC:UPI00000C1FEC; GB:AL139079; GB:AL111168; NID
A;Experimental source: serotype O2, strain NCTC 11168
C;Genetics:
A;Gene: Cj1728c

Query Match 1.6%; Score 7; DB 2; Length 51;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 SLVILGL 44
Db 19 SLVILGL 25
|||||

Search completed: June 6, 2006, 22:30:09
Job time : 44 secs

November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases; older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 6, 2006, 22:17:36 ; Search time 16 Seconds
(without alignments)
321.656 Million cell updates/sec

Title: US-10-063-537-32

Perfect score: 2315

Sequence: 1 MSGRDTILGLCILALSLA.....QDKHSLRNEEGTELOAIVR 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 58871 seqs, 11565156 residues

Total number of hits satisfying chosen parameters: 58871

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New*

- 1: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 3: /EMC_Celerra_SID33/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 4: /EMC_Celerra_SID33/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 5: /EMC_Celerra_SID33/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 6: /EMC_Celerra_SID33/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 7: /EMC_Celerra_SID33/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 8: /EMC_Celerra_SID33/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2315	100.0	445	6	US-10-196-749-148
2	2315	100.0	445	7	US-11-101-316-32
3	428	18.5	321	7	US-11-101-316-10
4	335.5	14.5	363	6	US-10-953-349-11171
5	326.5	14.1	353	6	US-10-953-349-11172
6	300.5	13.0	325	6	US-10-953-349-11173
7	222	9.6	366	6	US-10-953-349-17831
8	192.5	8.3	305	6	US-10-953-349-17832
9	187.5	8.1	281	6	US-10-953-349-17833
10	111	4.8	462	6	US-10-953-349-7915
11	111	4.8	482	6	US-10-953-349-7914
12	111	4.8	488	6	US-10-953-349-7913
13	97	4.2	691	6	US-10-511-937-2995
14	95.5	4.1	426	6	US-10-953-349-29132
15	95	4.1	426	6	US-10-953-349-2596
16	95	4.1	649	6	US-10-953-349-2595
17	95	4.1	667	6	US-10-953-349-2594
18	91	3.9	355	6	US-10-953-349-31241
19	90	3.9	352	6	US-10-953-349-29133
20	89.5	3.9	366	6	US-10-953-349-30070
21	89.5	3.9	376	6	US-10-953-349-30069
22	89.5	3.9	418	6	US-10-953-349-10300
23	89.5	3.9	425	6	US-10-953-349-30068
24	89.5	3.9	440	6	US-10-953-349-10299
25	89.5	3.9	475	6	US-10-953-349-10298

RESULT 1

US-10-196-749-148
; Sequence 148, Application US/10196749
; Publication No. US20060094864A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430RIC340
; CURRENT APPLICATION NUMBER: US/10/196,749
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 148
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-196-749-148

ALIGNMENTS

26	87.5	3.8	351	6	US-10-953-349-24340	Sequence 24340, A
27	86.5	3.7	344	6	US-10-994-679-9	Sequence 9, Appli
28	84.5	3.7	458	7	US-11-217-529-3	Sequence 3, Appli
29	83.5	3.6	372	6	US-10-953-349-11418	Sequence 11418, A
30	83.5	3.6	423	6	US-10-953-349-22475	Sequence 22475, A
31	83.5	3.6	459	6	US-10-953-349-11417	Sequence 11417, A
32	83.5	3.6	481	6	US-10-953-349-22474	Sequence 22474, A
33	83.5	3.6	499	6	US-10-953-349-11416	Sequence 11416, A
34	83	3.6	319	6	US-10-953-349-29134	Sequence 29134, A
35	83	3.6	536	6	US-10-953-349-27707	Sequence 27707, A
36	83	3.6	538	6	US-10-953-349-27706	Sequence 27706, A
37	83	3.6	554	6	US-10-953-349-27705	Sequence 27705, A
38	83	3.6	1205	6	US-10-953-349-4547	Sequence 4547, Ap
39	83	3.6	1243	6	US-10-953-349-4546	Sequence 4546, Ap
40	83	3.6	1286	6	US-10-953-349-4545	Sequence 4545, Ap
41	83	3.6	1503	7	US-11-312-958-48	Sequence 48, Appl
42	82.5	3.6	504	7	US-11-293-697-2761	Sequence 2761, Ap
43	82	3.5	235	6	US-10-953-349-12434	Sequence 12434, A
44	82	3.5	313	6	US-10-953-349-15450	Sequence 15450, A
45	82	3.5	327	6	US-10-953-349-15449	Sequence 15449, A

Query Match 100.0%; Score 2315; DB 6; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.5e-187;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGRDILGICILALALSAMMTFRFTITLLVHIFISVLIGLLFVCGVLMWLYDYTN 60
DB 1 MSGRDILGICILALALSAMMTFRFTITLLVHIFISVLIGLLFVCGVLMWLYDYTN 60

QY 61 DLSIELDTERENMKCVLGFATVSTGITAVLLVLI FVLRKRKIKLTVELFOITNKAISSAPF 120
DB 61 DLSIELDTERENMKCVLGFATVSTGITAVLLVLI FVLRKRKIKLTVELFOITNKAISSAPF 120

QY 121 LFPQPLWTFAILIFFVWLVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMSYHLIGLI 180
DB 121 LFPQPLWTFAILIFFVWLVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMSYHLIGLI 180

QY 181 WTSEFILAQQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILFFYHOGTVVKGSLISVV 240
DB 181 WTSEFILAQQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILFFYHOGTVVKGSLISVV 240

QY 241 RIPRIIWMYQNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVTTTAINGTDFC 300
DB 241 RIPRIIWMYQNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVTTTAINGTDFC 300

QY 301 TSAKDAFKILSKNSSHTSINCFDGFIIIFLGKVLVVCFTVFGGLMAFNYNRAFOQWAVPL 360
DB 301 TSAKDAFKILSKNSSHTSINCFDGFIIIFLGKVLVVCFTVFGGLMAFNYNRAFOQWAVPL 360

QY 361 LLVAFAYLVAHSFSLVFETVLDALFLCPAVDLETDGSEKPYFMDQEFSLFVKESNKL 420
DB 361 LLVAFAYLVAHSFSLVFETVLDALFLCPAVDLETDGSEKPYFMDQEFSLFVKESNKL 420

QY 421 NNARAQQDKSLRNEEGTELOAIVR 445
DB 421 NNARAQQDKSLRNEEGTELOAIVR 445

RESULT 2
US-11-101-316-32
; Sequence 32, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 32
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-101-316-32

Query Match 100.0%; Score 2315; DB 7; Length 445;

Best Local Similarity 100.0%; Pred. No. 1.5e-187;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGRDILGICILALALSAMMTFRFTITLLVHIFISVLIGLLFVCGVLMWLYDYTN 60
DB 1 MSGRDILGICILALALSAMMTFRFTITLLVHIFISVLIGLLFVCGVLMWLYDYTN 60

QY 61 DLSIELDTERENMKCVLGFATVSTGITAVLLVLI FVLRKRKIKLTVELFOITNKAISSAPF 120
DB 61 DLSIELDTERENMKCVLGFATVSTGITAVLLVLI FVLRKRKIKLTVELFOITNKAISSAPF 120

QY 121 LFPQPLWTFAILIFFVWLVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMSYHLIGLI 180
DB 121 LFPQPLWTFAILIFFVWLVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMSYHLIGLI 180

QY 181 WTSEFILAQQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILFFYHOGTVVKGSLISVV 240
DB 181 WTSEFILAQQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILFFYHOGTVVKGSLISVV 240

QY 241 RIPRIIWMYQNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVTTTAINGTDFC 300
DB 241 RIPRIIWMYQNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVTTTAINGTDFC 300

QY 301 TSAKDAFKILSKNSSHTSINCFDGFIIIFLGKVLVVCFTVFGGLMAFNYNRAFOQWAVPL 360
DB 301 TSAKDAFKILSKNSSHTSINCFDGFIIIFLGKVLVVCFTVFGGLMAFNYNRAFOQWAVPL 360

QY 361 LLVAFAYLVAHSFSLVFETVLDALFLCPAVDLETDGSEKPYFMDQEFSLFVKESNKL 420
DB 361 LLVAFAYLVAHSFSLVFETVLDALFLCPAVDLETDGSEKPYFMDQEFSLFVKESNKL 420

QY 421 NNARAQQDKSLRNEEGTELOAIVR 445
DB 421 NNARAQQDKSLRNEEGTELOAIVR 445

RESULT 3
US-11-101-316-10
; Sequence 10, Application US/11101316
; Publication No. US20060099657A1
; GENERAL INFORMATION:
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: ANTIBODIES TO A POLYPEPTIDE ENCODED BY A NUCLEIC ACID
; FILE REFERENCE: P3230R1C17C1
; CURRENT APPLICATION NUMBER: US/11/101,316
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: 10/063526
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 10/006867
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 10
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-101-316-10

Query Match 18.5%; Score 428; DB 7; Length 321;
Best Local Similarity 34.6%; Pred. No. 4e-29;
Matches 91; Conservative 55; Mismatches 93; Indels 24; Gaps 6;

```

QY 174 YHILGLIWTSEFILACQMTIAGAVTCYENRSK-NDPPDHPILSSLSILFFHQGTQVVK 232
Db 56 YGVLGLFTLWNLVGLQCVLAGAFASFYWAFHKQDIPFPLISAFIRTLRYHTGSLAF 115
QY 233 GSFLISVVRIPRIIVMYMNALEQOQHGSLSRYLFCYCCYCFWCLDKYLLHLNQNAYTTT 292
Db 116 GAULITLVQIARVILEYIDHKLGVQN-PVARCIMCCFKCLWCLKLEKFIKFLNRNAYIMI 174
QY 293 AINGTDFCTSAKDAFKILSKNSHFTSINCFGDFIIFLGLKLVV-----CFTVFGGLMA 346
Db 175 AIYGNKFCVAKNAFMLLMENVRVVLDKVTDLFFGLLVGGVGVLSFFFSGRIP 234
QY 347 -----FNNRAPOQWAVPVLVLAFFAYLVHVSFLSVFETVLDALFLCAVDLETN 396
Db 235 GLGKDFKSPHLN-----YV-LPIMTSILGAYVIASGFFSVFGMVCVDTLFLCFLEDLERN 288
QY 397 DGSSEKPYFMDQFSLPVKESNK 419
Db 289 NGSLDRPYNKSLLKILGKNE 311

RESULT 4
US-10-953-349-11171
; Sequence 11171, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11171
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-11171
Query Match 14.5%; Score 335.5; DB 6; Length 363;
Best Local Similarity 27.8%; Pred. No. 2.7e-21;
Matches 95; Conservative 63; Mismatches 137; Indels 47; Gaps 11;

QY 99 KRILKTVLQITNKAISSAPFLLFQPLWTFAILFPFWLVAVLLSLGTAGAAQVME-- 156
Db 7 RRLMATSVLKVAKVIGEVOALIIFPAIFAMLAIFYMFWISAALHLFSSG--QVQNN 64
QY 157 -----GGQVEYKPLSGIRYMWSYHLGLIWTSEFILACQOMTI 194
Db 65 CNNTNCCAYDLVLKVNCDRCGYSIHYTPTHTIAIF--FHLFGCYWATQFFIASSATVI 122
QY 195 AGAVTCYFNRSKNDP--PDHPILSSLSILFFHQGTQVKGSLISVVRIPRIIVMYM 252
Db 123 AGSVASYWAQGEASPEIFLPVFAFMKRLARYNLGSLVSLVSVESVRFLEAIRR 182
QY 253 ALK-----BQOHGALSRYLFR--CCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKD 305
Db 183 KTVSGTIPDHWFRMAHYTSRGLSKSVETIKS-----VNRNAYIMIAITGSKFSKSAI 238
QY 306 AFKILSKNSHFTSINCFGDFIIFLGLKLVVCF--VFGGLM--AFNYNRAFOQWAVPVL- 361
Db 239 ATELIISNLRIGKVNVIQVILFGLKCLVSLFSAFGFLMLDSHRYRASHNKVSSPLP 298
QY 362 LVAFPA--YLVAFSFLSVFETVLDALFLCAVDLETNDGSSE 401
Db 299 VLACWALGYIVATLFFAVVEMSIDTIILSFQDSEENQGNQAQ 340

RESULT 5
US-10-953-349-11172
; Sequence 11172, Application US/10953349

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; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11172
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-11172
Query Match 14.1%; Score 326.5; DB 6; Length 353;
Best Local Similarity 27.5%; Pred. No. 1.5e-20;
Matches 93; Conservative 62; Mismatches 136; Indels 47; Gaps 11;

QY 103 LTVLQITNKAISSAPFLLFQPLWTFAILFPFWLVAVLLSLGTAGAAQVME----- 156
Db 1 MATSVLKVAKVIGEVOALIIFPAIFAMLAIFYMFWISAALHLFSSG--QVQNNCNT 58
QY 157 -----GGQVEYKPLSGIRYMWSYHLGLIWTSEFILACQOMTIAGAV 198
Db 59 NCCAYDLVLKVNCDRCGYSIHYTPTHTIAIF--FHLFGCYWATQFFIASSATVIAGSV 116
QY 199 VTCYFNRSKNDP--PDHPILSSLSILFFHQGTQVKGSLISVVRIPRIIVMYMNAK- 255
Db 117 ASYWAQGEASPEIFLPVFAFMKRLARYNLGSLVSLVSVESVRFLEAIRRKT 176
QY 256 -----BQOHGALSRYLFR--CCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKI 309
Db 177 SGTIPDHWFRMAHYTSRGLSKSVETIKS-----VNRNAYIMIAITGSKFSKSAIATEL 232
QY 310 LSKNSHFTSINCFGDFIIFLGLKLVVCF--VFGGLM--AFNYNRAFOQWAVPVL-LVAF 365
Db 233 IISNLRIGKVNVIQVILFGLKCLVSLFSAFGFLMLDSHRYRASHNKVSSPLPVLAC 292
QY 366 FA--YLVAFSFLSVFETVLDALFLCAVDLETNDGSSE 401
Db 293 WALGYIVATLFFAVVEMSIDTIILSFQDSEENQGNQAQ 330

RESULT 6
US-10-953-349-11173
; Sequence 11173, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11173
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-11173
Query Match 13.0%; Score 300.5; DB 6; Length 325;
Best Local Similarity 28.1%; Pred. No. 2.1e-18;
Matches 87; Conservative 57; Mismatches 119; Indels 47; Gaps 11;

QY 131 ILIFFPWLWVAVLLSLGTAGAAQVME-----GGQVEYKPLS 166
Db 1 MLAIYMFWISAALHLFSSG--QVQNNCNTNCCAYDLVLKVNCDRCGYSIHYTPHI 58
QY 167 GIRYMWSYHLGLIWTSEFILACQOMTIAGAVTCYFNRSKNDP--PDHPISSLSILFF 224

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Db	59	TIA	TF	--	FHL	FGC	WAT	OFF	FT	ASS	TV	AGS	VAS	YWA	QGE	AS	PI	PI	PL	PL	VF	AS	MK	RL	AR	116																																	
Qy	225	YH	QGT	VV	KG	S	FL	I	SV	VR	PI	RI	IV	MY	M	Q	N	A	L	K	----	E	Q	H	G	A	L	S	RY	L	FR	--	C	Y	C	F	W	C	177																				
Db	117	Y	N	L	G	S	V	A	L	G	S	I	V	F	V	S	R	F	I	L	E	A	I	R	B	K	T	V	G	S	T	P	D	H	W	F	R	M	A	H	Y	T	S	R	G	C	L	K	S	V	E	W	T	176					
Qy	278	D	K	L	L	H	L	N	O	N	A	T	T	T	T	A	I	N	G	T	O	P	C	T	S	A	K	A	F	L	K	S	N	S	H	F	T	S	I	N	C	F	G	D	P	I	F	L	G	K	V	L	V	V	C	337			
Db	177	K	S	----	V	N	R	A	Y	I	M	A	I	T	A	I	T	G	K	S	F	K	S	S	A	T	E	L	I	I	S	N	I	L	R	I	G	K	V	N	V	I	G	D	V	I	L	F	L	G	K	L	C	V	S	L	232		
Qy	338	F	T	--	V	F	G	G	L	M	----	A	F	N	V	N	R	A	F	O	W	A	V	P	L	L	--	L	V	A	P	F	A	--	Y	L	V	A	H	S	F	L	S	V	F	E	T	V	L	D	A	L	F	L	C	P	A	V	391
Db	233	F	S	A	L	F	G	F	L	M	L	D	S	H	R	Y	R	A	S	H	N	K	V	S	S	P	L	L	P	V	L	C	A	W	A	L	G	I	V	A	T	L	F	F	A	V	E	M	S	I	D	T	I	I	L	S	F	Q	292
Qy	392	D	L	E	T	N	D	G	S	E	401																																																
Db	293	D	S	E	E	N	O	G	N	A	O	302																																															

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RESULT 7
US-10-953-349-17831
; Sequence 17831, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17831
; LENGTH: 366
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-17831

```

RESULT 8

US-10-953-349-17832
; Sequence 17832, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579FUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17832
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-17832

```

RESULT 9
US-10-953-349-17833
; Sequence 17833, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17833
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-17833

```

	Query Match	8.1%	Score 187.5	DB 6	Length 281
	Best Local Similarity	23.2%	Pred. No. 5.6e-09		
	Matches 58	Conservative 53	Mismatches 114	Indels 25	Gaps 7
Qy	157	GGQVEKPLSGIRYMWSYHLIGLWTSFEFLACQOQMTIAGAVVTCYPNRSKNDDPDHPIIL	216		
Db	18	GDCENKEDSWPAYVALAVLTMLWAAAAMVEAQVVTISGTIANWYFSK- EHOTPKRSIR	76		
Qy	217	SSLSLIFFYHOGVTKVGSFLISVVVRIPIRIIVTMQNALKEQQGALSRYLFRCCYCCFCWC	276		
Db	77	TPLRNVFGPSGGTTCISGLVCVVRWVSAY ---DSARQEDTGVIVNLV ---RCCVNA	129		

Qy 277 LDKYLLHNNQAYTTTAINGTDFCTSAKDAPKILSKNSSHTFSINCFG-----FIIF 329
Db 130 LLTAVDFLNKPTINFAAITGEAYCSSARMYTELLRRNLISAVFVETISSRILAGIVFVS 189
Qy 330 LGKVLVCTFTVFG--LMAFNTRAFQWAVPELLVAFFAYLVAHSFLSVFETVLDAFL 387
Db 190 ASYTVACVILKAGTNGLSDSYFAAMAW---VLLMVLGVLY----HVLNDVIDTIYV 241
Qy 388 CFAVDLETND 397
Db 242 CYAIDRDRE 251

```

RESULT 10
US-10-953-349-7915
; Sequence 7915, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7915
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-7915

```

Query Match	4.8%;	Score 111;	DB 6;	Length 462;
Best Local Similarity	18.9%;	Pred: No. 0.026;		
Matches	78;	Conservative	72;	Mismatches 171; Indels 92; Gaps 16;
Qy	13	LALALSLAMMTFFRPIITLLVHIP-----	ISLVILGLLFVCGVLWMLWLYDYTDNDL	62
Db	45	LTLSLLVILVITIRGLISASTHHFHLKKWYPELLASVAVSG--IASLWQOCIFYNPSR	101	
Qy	63	SIEDTERENMKCVLGFPAIVSGITAVLLVLI-----	FVLKRRIKLTWELF----	108
Db	102	AV-----KATFWLSPILITCSVIGLLVLIGSADVADIGAVFVL---	FAITQSLYGCW	149
Qy	109	-----QITNKAISSAPFLFLOPLMTFALLIEFFWLWVAVLLSLCTAGAAQVMEGGQVEYK	163	
Db	150	ITPRLLEYTDKILSLA--TAFPPARTRE-----	VVCLSIIVSVYVSGFLVTGIGASTR	201
Qy	164	PLSGIRYMWSHLIGLIWTSBFILACQOMTIAGAVVTCYFNRSKNDDPDHPHILSSLSILF	223	
Db	202	TNLDILFI-SVIIISLAWTMQVKNVQOVALISRA---RYNVFAHGE--DMDANAFRITM	255	
Qy	224	FYHOGTVVKGSGFLISVVRIPRIIWMYQNALK--EQQHGALSRYLFCRCYCCFWCLDKYL	281	
Db	256	KHLTGSICVGSNTLP-----	IVIFKGSIRSVNLMSSGDEVMYSGADCFSTIAKKLI	308
Qy	282	LHLNQNAVYTTTAINGTDFTCSAKDAFKILSKNS-----	SHFTSINCF-----	323
Db	309	TLGNRWGFVHVGTVDKGFMGEASSDWTKKFRSTTGLEKLIDSLTSSFCFLSAVSGVAVSS	368	
Qy	324	---GDFFILFLGKVLVVCVTVFGGLMAFNYNRAFQVWAVPLLVIAFFAYLVAHS	373	
Db	369	LTAGTWMLLIHKDALEYALTVAFIGYFVGRVGLAW-----	LOACVLAYIYAYS	417

RESULT 11
US-10-953-349-7914
; Sequence 7914, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

```

; TITLE OF INVENTION: ENCODED THERBY
;
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7914
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; US-10-953-349-7914

```

Query March	4.88;	Score 111;	DB 6;	Length 482;
Best Local Similarity	18.9%;	Pred. No. 0.027;		
Matches 78;	Conservative	72;	Mismatches 171;	Indels 92;
Gaps	16;			
QY	13	LALALSAMFTFRFIITLLVHIF-----ISLVILGLLFVCGVLWMLYYDYNDL	62	
DB	65	LTLISLVIVLTIRGLISASTHFFHLKKWYPLLASVAVSG--IASLAWQCIFYNPSR	121	
QY	63	SIELDTRENMKCVLGFPAIVSTGITAVLVLI-----FVLKRKRLTWELF---	108	
DB	122	AV-----KATFWLSPILTCVSGILLVLIGSAVDAGIAVFVL---FAITQSLYGCW	169	
QY	109	-----QITNKAISAPPELLQPLWTFAILFFWVLWAVLLSLCTAGAAQWMEGGQVEYK	163	
DB	170	ITPRLTYDKLSUA--TAPPARTRE-----VVCLSIIVSVYSGFLVTGIGGATSTR	221	
QY	164	PLSGIRYMWSYHLIGLIWTSEFILACQOMTIAGAVVTCYFNRRSKNDPPDHPILSSLSILF	223	
DB	222	TNLDILFI-SVLIISLAWTMQVIKNVQQAISRA---RYVNFAHGE--DMDAWNAPRITM	275	
QY	224	FYHOGTVVKGSGFLISVVRIIRLIWMYQNALK--EQOHGALSRYLFRCCYCCFWCLDKYL	281	
DB	276	KHLTGSICVSGSTLVP-----IIVFIRGIRSIVNLMSGSDVVMYSGADCFSTIANKLI	328	
QY	282	LHLNQNAYYTTAINGTDTCFSAKDAFKILSKNS-----SHETSINCF-----	323	
DB	329	TLGNRWGFMVHGTVDKGFMEASDWTKKFRSTTGLEKLI DSLTSSCFLSAVSVGVAVSS	388	
QY	324	---GDFIIFLGKVLUVCTFVGGUMAFNYNRAQVWAVPLLVLAFFAYIAVHS	373	
DB	389	LTAGIMMLLTHKDYALEVTLYAFIIGYFVGKVGGLW---LQACVLAYYVAYS	437	

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RESULT 12
US-10-953-349-7913
; Sequence 7913, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLY
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7913
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-7913

```

Query Match	4.8%	Score 111;	DB 6;	Length 488;	
Best Local Similarity	18.9%;	Pred. No. 0.027;			
Matches	78;	Conservative	72;	Mismatches 171;	Indels 92; Gaps 16;
QY	13	LALALSAMMETFEFITTLLVHF	-----	ISLVILGLLFCVGVWLWLYDYDNDL	62
DB	71	LTLSLVIVLTIRGLISASTHPLKKVPPLLASVAVSG	-----	IASLAWQCIFIIYPSR	127
QY	63	SIEDTERENMKCVGFIAVSTGHTAVLLVLI	-----	FVLKRKLIVTELF	108

Db 128 AV-----KATFWLSPLTSCVGLLVLIGSAVDAGIGAVFVL---FAITQSLYGCW 175
QY 109 -----QITNKAISSAPFLPQPLWTFAILFFWLMVAVLLSGTAGAAQWMEGGQVEYK 163
Db 176 ITPRELVTKILSLA--TAPPPARTRE-----VCLSIIVSVVYSGFLVTGIGGATSTR 227
QY 164 PLSGIRYMSYHLIGLWTSFILAQQMTIAGAVVTCYFNRSKNDPPDPHPILSSLSILF 223
Db 228 TNDJLIFI-SVIIISLAWTMQVINKVQVAISRA---RYNFAHGE--DMDAWNAPRITW 281
QY 224 FYHQGTWKGSLISVVRIPRIIVMYMOMNALKEQHGALSRYLFRCCYCCFWCLDKYL 281
Db 282 KHLTGSICVGTLP-----IIVIRGSIRSVNLMGSSDDEVYSGADCFSTIANKLI 334
QY 282 LHLNQAYTTAINGTDFCTSAKDAFKILSKNS-----SHTSINCF----- 323
Db 335 TLGNRWGFVHVGTYDKGFMEASSDTWKFKRSTTGLEKLI DSDLTSSFCFLSAVSGAVSS 394
QY 324 ---GDFFILGKVLVVCFTVFGGLMAFNYNRAFOVWAVPPLLVAFFAYLVAHS 373
Db 395 LTAGIWMLLIHKDYALEVTLYAFIIGYFVGRVGLW----LOACVLAYYVAYS 443

RESULT 13

US-10-511-937-2995
; Sequence 2995, Application US/10511937
; Publication No. US20060088836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000104
; CURRENT FILING DATE: 2004-10-19
; PRIOR FILING DATE: 2003-04-24
; PRIOR FILING DATE: 2003-04-24
; PRIOR FILING DATE: 2002-04-24
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2995
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2995

Query Match 4.2%; Score 97; DB 6; Length 691;
Best Local Similarity 18.2%; Pred. No. 0.6;
Matches 88; Conservative 70; Mismatches 166; Indels 160; Gaps 20;
QY 7 ILGLCTIALALSAMWTFRRFITTLLVHI-----FI 37
Db 92 ILSVLLTLPQHLVQLYFLTALLLYAGHQISRDYVRSELEFAYEGPMYLPNSNRF 151
QY 38 SLVILGLLFFCGVL-----WLYDYDNDLSIELD--TERENMKRCVLGFAIVSTGITA 88
Db 152 TTALIGLVVCTLCSCVMKTKQIWLFSAHMLPRLARCLVPLETIVILINKFAMIFTGLEV 211
QY 89 V-----LLVLI FVLKRKLTVELFQITNKAISSAPFLFPQPLWTF--FAILIFFWLVWA 141
Db 212 LYFLGNLLVPYNLAKSAVRELQVVEYVGL-----LALGMLWNQLVVFLVFWFLV 265
QY 142 VLLSLGTAGAAQWMEGGQVEYKPLSGIRYMW-----SYHLIGLWTSFILA 189

Db 266 LF-----ALQIYSVSTRDQASRERLLFLTSLIAECCSTPYSLGLGVFTSVF--- 315
QY 190 QQMTIAGAVVTCYF-----NRSKNDDPPHPILSS-----LS 220
Db 316 ----ALGVLTCLCKFYLGQYRAFNMNDPAMNRGTGVTLLILAVOTGLIELQVHVHRAFLLS 371
QY 221 ILFFVHQGTWKGSLISVVRIPRIIVMYMOMNALKEQHGALSRYLFRCCYCCFWCL--D 278
Db 372 IILF-----IVVASILQSMLEIADPVL---ALGASRDKSLWKH--FRAVSLCLFLVLP 421
QY 279 KYLLHLNQAYTTAINGTDFCTSAKDAFKILSKNSSHFTSINCFGDFIIFL----- 330
Db 422 AYM-----AYMCOFFHMF-----WLLIISSILTSLOVLGTLFIYVLEWVEER 468
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QY 375 LSVF 378
Db 524 YNWM 527

RESULT 14

US-10-953-349-29132
; Sequence 29132, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCODED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 29132
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-29132

Query Match 4.1%; Score 95.5; DB 6; Length 446;
Best Local Similarity 22.2%; Pred. No. 0.5;
Matches 93; Conservative 52; Mismatches 156; Indels 117; Gaps 22;
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Db 78 GLIFFVGVAVW-----RVVAAEMGVGGEKFPQGTGVALGLSVWS----SVSIV----- 121
QY 99 KRKLTVELFOITNKAI--SSAPFLPQPLWTFAILFFWLMVAVLLSL-----GTA 149
Db 122 -----ICNKALMSSLGTFATLTLSWHLLVTFCSLHVLMKFEHKAFAFSRTV 170
QY 150 GAAQWMEGGQVEYKPLS--GIRYMWVSYHLI GLIWTSEFILACQOMTIAGAVVTCYFNRSKN 208
Db 171 MFGVLNGISIGLNLNLSGFNSGVFQM-----TKLAIPTCT-----VILETLFRKKF 219
QY 209 DPPDPHFLSSLSILFFPYHOGTVVK-----GSFLISVVRIPRIIVMYMOMNALKEQ 258
Db 220 ---SRTIQISLSVLL--GUGVATWTDLQNLNAGSILSLLAIITTCIAQIMTNTQKKF 273
QY 259 HGALSRYLFRCC-----YCCFWCLDKYLLHLNQAYTTAINGTDFCTSAKDAFKILS 311
Db 274 KVSSTOLLYQSCPQSLTLFLIGPDLGFL--TNQNVAFNFTYNSNVF-----FIVLS 324
QY 312 KNSSHFTSINCFGDFIIFLGKVLVWCFTVFGGLMAFNYNRAFOVWAVPPLLVAFFAYLVA 371
Db 325 CLIS--VSN--FSTFLV--IGKTSPTYQVLGHKT-----CLVLTFCGVLL 366
QY 372 HSFLSVFETVLDALFLCFADVLETNDGSEKPYFMDQBFSLFVKRNKLNARAQODK 429

Search completed: June 6, 2006, 22:20:59
Job time : 17 secs

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OM protein - protein search, using sw model

Run on: June 8, 2006, 23:59:01 ; Search time 186 Seconds
(without alignments)
1108.229 Million cell updates/sec

Perfect score: 2315

Sequence: 1 MSGRDTILGICILALSLA.....QQDKSLRNEEGTELQAIVR 445

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Published Applications AA Main:

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- 2: /EMC_Celerra_SID33/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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562	2315	100.0	445	4	US-10-174-587-148 Sequence 148, App
626	2315	100.0	445	4	US-10-063-742-32 Sequence 32, Appl
741	2315	100.0	445	5	US-10-972-317-32 Sequence 32, Appl
743	2315	100.0	445	5	US-10-950-374-177 Sequence 177, App
751	2315	100.0	445	6	US-11-102-240-32 Sequence 32, Appl
752	2315	100.0	445	6	US-11-103-195-32 Sequence 32, Appl
753	2314	99.9	653	4	US-10-062-937B-5 Sequence 5, Appli
754	2314	99.9	653	4	US-10-391-399-73 Sequence 73, Appl
755	2280.5	98.5	648	5	US-10-330-773-825 Sequence 825, App
756	1696.5	73.3	558	5	US-10-330-773-822 Sequence 822, App
757	1456	62.9	275	3	US-09-833-245-1911 Sequence 1911, Ap
758	1456	62.9	275	6	US-11-264-096-1911 Sequence 1911, Ap
759	1443	62.3	275	3	US-09-833-245-1910 Sequence 1910, Ap
760	1443	62.3	275	6	US-11-264-096-1910 Sequence 1910, Ap
761	1132	48.9	653	4	US-10-062-937B-9 Sequence 9, Appli
762	1132	48.9	653	4	US-10-391-399-77 Sequence 77, Appl
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764	1121	48.4	654	4	US-10-391-399-75 Sequence 48, Appl
765	1121	48.4	657	4	US-10-176-847-48 Sequence 6, Appli
766	1121	48.4	657	5	US-10-753-267-6 Sequence 48, Appl
767	1121	48.4	657	6	US-11-080-991-48 Sequence 48, Appl
768	1121	48.4	708	4	US-10-106-698-6390 Sequence 6390, Ap
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773	1107	47.8	446	5	US-10-919-142-58 Sequence 58, Appl

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783	593.5	25.6	695	4	US-10-139-496-4 Sequence 4, Appli
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785	589.5	25.5	706	4	US-10-062-937B-8 Sequence 8, Appli
786	589.5	25.5	706	4	US-10-139-496-2 Sequence 2, Appli
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788	589.5	25.5	706	4	US-10-391-399-76 Sequence 76, Appl
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792	577.5	24.9	698	5	US-10-417-375-84 Sequence 84, Appl
793	577.5	24.9	698	5	US-10-417-375-88 Sequence 88, Appl
794	576.5	24.9	690	4	US-10-210-172-24 Sequence 24, Appl
795	568	24.5	717	4	US-10-062-937B-2 Sequence 2, Appli
796	568	24.5	717	4	US-10-391-399-70 Sequence 70, Appl
797	568	24.5	717	4	US-10-768-158-26 Sequence 26, Appl
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840	524	22.6	722	4	US-10-306-631-103 Sequence 103, App
841	524	22.6	722	4	US-10-306-631-105 Sequence 105, App
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843	517	22.3	403	6	US-11-072-512-2454 Sequence 2454, Ap
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850	452	19.5	598	4	US-10-306-631-97	Sequence 97, Appl	1142	107	4.6	345	4	US-10-359-285-5	Sequence 5, Appl1
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1118	112.5	4.9	348	4	US-10-081-810-54	Sequence 54, Appl	1191	100.5	4.3	373	4	US-10-228-667-2	Sequence 2, Appl1
1119	112.5	4.9	348	4	US-10-278-087A-46	Sequence 46, Appl	1192	100.5	4.3	373	4	US-10-145-586-28	Sequence 28, Appl
1120	111.5	4.8	339	4	US-10-087-192-1467	Sequence 1467, Ap	1193	100.5	4.3	373	5	US-10-935-190-16	Sequence 16, Appl
1121	111.5	4.8	834	4	US-10-017-161-2412	Sequence 2412, Ap	1194	100.5	4.3	373	5	US-10-237-813-4	Sequence 4, Appl1
1122	109.5	4.7	834	4	US-10-017-161-1996	Sequence 1996, Ap	1195	100.5	4.3	611	5	US-10-505-486-67	Sequence 67, Appl
1123	108.5	4.7	345	4	US-10-262-313-11	Sequence 11, Appl	1196	100.5	4.3	862	6	US-11-097-143-5382	Sequence 5382, Ap
1124	108.5	4.7	345	4	US-10-254-905-10	Sequence 10, Appl	1197	100.5	4.3	391	4	US-10-282-122A-48531	Sequence 48531, A
1125	108.5	4.7	345	4	US-10-768-878-11	Sequence 11, Appl	1198	100	4.3	403	4	US-10-282-122A-49552	Sequence 49552, A
1126	108.5	4.7	346	2	US-08-999-112-32	Sequence 32, Appl	1199	100	4.3	490	6	US-11-079-463-5351	Sequence 5351, Ap
1127	108.5	4.7	346	3	US-09-966-782A-10	Sequence 10, Appl	1200	100	4.3	371	4	US-09-905-253A-4	Sequence 4, Appl1
1128	108.5	4.7	346	3	US-09-992-331-11	Sequence 11, Appl	1201	99.5	4.3	371	4	US-10-201-187-4	Sequence 4, Appl1
1129	108.5	4.7	346	3	US-09-825-751A-83	Sequence 83, Appl	1202	99.5	4.3	371	4	US-10-603-566-4	Sequence 4, Appl1
1130	108.5	4.7	346	3	US-09-771-287-5	Sequence 5, Appl1	1203	99.5	4.3	371	5	US-10-893-485-4	Sequence 4, Appl1
1131	108.5	4.7	346	4	US-10-212-980-6	Sequence 6, Appl1	1204	99.5	4.3	371	5	US-10-237-813-5	Sequence 5, Appl1
1132	108.5	4.7	346	4	US-10-007-132-5	Sequence 5, Appl1	1205	99.5	4.3	371	6	US-11-134-811-4	Sequence 4, Appl1
1133	108.5	4.7	346	4	US-10-006-343-5	Sequence 5, Appl1	1206	99.5	4.3	371	6	US-11-218-281-2	Sequence 2, Appl1
1134	108.5	4.7	346	4	US-10-298-992-7	Sequence 7, Appl1	1207	99.5	4.3	371	6	US-11-218-281-33	Sequence 33, Appl
1135	108.5	4.7	346	4	US-10-285-019-30	Sequence 30, Appl	1208	99.5	4.3	342	6	US-11-098-686-10521	Sequence 10521, A
1136	108.5	4.7	346	4	US-10-466-205-1	Sequence 1, Appl	1209	99	4.3	371	4	US-09-905-253A-2	Sequence 2, Appl1
1137	108.5	4.7	346	4	US-10-240-801A-11	Sequence 11, Appl	1210	99	4.3	371	4	US-10-201-187-2	Sequence 2, Appl1
1138	108.5	4.7	346	5	US-10-851-438-83	Sequence 83, Appl	1211	99	4.3	371	4	US-10-201-187-2	Sequence 2, Appl1

1212	99	4.3	371	4	US-10-225-567A-235	Sequence 235, App	1285	96.5	4.2	613	4	US-10-251-385-92	Sequence 92, Appl
1213	99	4.3	371	4	US-10-282-798-664	Sequence 664, App	1286	96.5	4.2	953	4	US-10-128-714-3297	Sequence 3297, App
1214	99	4.3	371	4	US-10-603-566-2	Sequence 2, Appl	1287	96.5	4.2	954	4	US-10-437-963-204079	Sequence 204079, App
1215	99	4.3	371	5	US-10-753-267-128	Sequence 128, App	1288	96.5	4.2	1056	4	US-10-128-714-8297	Sequence 8297, App
1216	99	4.3	371	5	US-10-893-485-2	Sequence 2, Appl	1289	96	4.1	244	4	US-10-437-963-153664	Sequence 153664, App
1217	99	4.3	371	6	US-10-237-813-3	Sequence 3, Appl	1290	96	4.1	338	4	US-10-343-650A-678	Sequence 678, App
1218	99	4.3	371	6	US-11-134-811-2	Sequence 2, Appl	1291	96	4.1	416	4	US-10-335-977-5911	Sequence 5911, App
1219	99	4.3	373	6	US-11-218-281-1	Sequence 1, Appl	1292	96	4.1	421	4	US-10-335-977-5912	Sequence 5912, App
1220	99	4.3	373	6	US-11-218-281-28	Sequence 2, Appl	1293	96	4.1	438	4	US-10-282-122A-55742	Sequence 55742, App
1221	99	4.3	385	5	US-10-617-320-1643	Sequence 463, App	1294	96	4.1	670	4	US-10-282-122A-69771	Sequence 69771, App
1222	99	4.3	611	5	US-10-505-486-90	Sequence 90, Appl	1295	96	4.1	786	4	US-10-424-599-254383	Sequence 254383, App
1223	99	4.3	788	4	US-10-322-281-663	Sequence 663, App	1296	96	4.1	2288	4	US-10-736-883-40	Sequence 40, Appl
1224	98.5	4.3	394	4	US-10-282-122A-78100	Sequence 78100, A	1297	95.5	4.1	393	4	US-10-282-122A-43114	Sequence 43114, A
1225	98.5	4.3	442	4	US-10-282-122A-58720	Sequence 58720, A	1298	95	4.1	232	4	US-10-276-774-1924	Sequence 1924, App
1226	98.5	4.3	485	4	US-10-369-493-18121	Sequence 18121, A	1299	95	4.1	308	4	US-10-017-161-692	Sequence 692, App
1227	98.5	4.3	485	5	US-10-732-923-23457	Sequence 23457, A	1300	95	4.1	318	5	US-10-793-626-3118	Sequence 3118, App
1228	98.5	4.3	496	6	US-11-097-143-11013	Sequence 11013, A	1301	95	4.1	319	4	US-10-231-079-21	Sequence 21, Appl
1229	98.5	4.3	695	4	US-10-042-865-138	Sequence 138, App	1302	95	4.1	319	4	US-10-292-798-604	Sequence 604, App
1230	98.5	4.3	695	4	US-10-072-012-397	Sequence 397, App	1303	95	4.1	319	4	US-10-311-196-10	Sequence 10, Appl
1231	98	4.2	318	3	US-09-800-274-6	Sequence 6, Appl	1304	95	4.1	319	5	US-10-511-538-21	Sequence 21, Appl
1232	98	4.2	318	4	US-10-252-798-1732	Sequence 1732, App	1305	95	4.1	484	6	US-11-188-298-18146	Sequence 18146, A
1233	98	4.2	318	4	US-10-724-208-4	Sequence 4, Appl	1310	94.5	4.1	437	6	US-11-079-463-8067	Sequence 8067, App
1234	98	4.2	318	4	US-10-755-889-600	Sequence 30, Appl	1306	95	4.1	530	4	US-10-724-972A-5048	Sequence 5048, App
1235	98	4.2	318	5	US-10-756-149-5650	Sequence 600, App	1307	94.5	4.1	294	4	US-10-282-122A-44615	Sequence 44615, A
1236	98	4.2	318	6	US-11-127-877-38	Sequence 38, Appl	1308	94.5	4.1	387	5	US-10-793-626-3180	Sequence 3180, App
1237	98	4.2	321	3	US-09-825-882-4	Sequence 4, Appl	1309	94.5	4.1	416	4	US-10-282-122A-63267	Sequence 63267, A
1238	98	4.2	321	4	US-10-282-798-1732	Sequence 1732, App	1310	94.5	4.1	437	6	US-11-079-463-8067	Sequence 8067, App
1239	98	4.2	321	4	US-10-724-208-4	Sequence 4, Appl	1311	94.5	4.1	437	6	US-11-079-463-8067	Sequence 8067, App
1240	98	4.2	321	5	US-10-770-127-175	Sequence 175, App	1312	94.5	4.1	701	5	US-10-450-763-38967	Sequence 38967, A
1241	98	4.2	321	5	US-10-724-209-4	Sequence 4, Appl	1313	94.5	4.1	735	4	US-10-437-963-162148	Sequence 162148, App
1242	98	4.2	321	5	US-10-986-871-4	Sequence 4, Appl	1314	94.5	4.1	741	5	US-10-450-763-55419	Sequence 55419, A
1243	98	4.2	321	5	US-10-017-161-2086	Sequence 2086, App	1315	94.5	4.1	857	6	US-11-052-554A-218	Sequence 218, App
1244	98	4.2	338	4	US-10-017-161-2140	Sequence 2140, App	1316	94	4.1	49	4	US-10-062-937B-12	Sequence 12, Appl
1245	98	4.2	338	4	US-10-292-798-1786	Sequence 1786, App	1317	94	4.1	49	4	US-10-391-399-80	Sequence 80, Appl
1246	98	4.2	338	4	US-10-343-650A-678	Sequence 678, App	1318	94	4.1	335	4	US-10-333-946-11	Sequence 11, Appl
1247	98	4.2	486	5	US-10-617-320-4466	Sequence 4466, App	1319	94	4.1	340	3	US-09-791-932-117	Sequence 117, App
1248	98	4.2	486	4	US-10-724-972A-4076	Sequence 4076, App	1320	94	4.1	340	3	US-09-990-940-2	Sequence 2, Appl
1249	98	4.2	642	4	US-10-282-122A-51332	Sequence 51332, A	1321	94	4.1	340	3	US-09-564-923A-2	Sequence 2, Appl
1250	98	4.2	663	3	US-09-815-242-10070	Sequence 10070, A	1322	94	4.1	340	4	US-10-225-567A-666	Sequence 666, App
1251	98	4.2	663	4	US-10-287-274-332	Sequence 332, App	1323	94	4.1	340	4	US-10-291-990-29	Sequence 29, Appl
1252	97.5	4.2	663	4	US-10-282-122A-56452	Sequence 56452, A	1324	94	4.1	340	4	US-10-321-807-40	Sequence 40, Appl
1253	97.5	4.2	250	4	US-10-282-122A-62825	Sequence 62825, A	1325	94	4.1	340	4	US-10-332-082-3	Sequence 3, Appl
1254	97.5	4.2	250	4	US-10-282-122A-64530	Sequence 64530, A	1326	94	4.1	340	4	US-10-472-629-3	Sequence 3, Appl
1255	97.5	4.2	373	4	US-10-225-567A-402	Sequence 402, App	1327	94	4.1	340	4	US-10-478-534-4	Sequence 4, Appl
1256	97.5	4.2	374	4	US-10-242-499-3	Sequence 3, Appl	1328	94	4.1	340	4	US-10-321-807-40	Sequence 40, Appl
1257	97.5	4.2	454	5	US-10-793-626-1516	Sequence 1516, App	1329	94	4.1	340	4	US-10-314-048A-40	Sequence 40, Appl
1258	97.5	4.2	454	4	US-10-335-977-6163	Sequence 6163, App	1330	94	4.1	340	4	US-10-477-985-58	Sequence 58, Appl
1259	97.5	4.2	456	4	US-10-335-977-6164	Sequence 6164, App	1331	94	4.1	340	4	US-10-680-402-2	Sequence 2, Appl
1260	97.5	4.2	512	3	US-09-962-290-2	Sequence 2, Appl	1332	94	4.1	340	5	US-10-897-815-40	Sequence 40, Appl
1261	97.5	4.2	663	4	US-10-282-122A-78152	Sequence 78152, A	1333	94	4.1	340	5	US-10-500-672-37	Sequence 37, Appl
1262	97	4.2	335	4	US-10-278-455-4	Sequence 4, Appl	1334	94	4.1	340	5	US-10-941-486-5	Sequence 5, Appl
1263	97	4.2	335	4	US-10-278-437-4	Sequence 4, Appl	1335	94	4.1	340	5	US-10-930-662-40	Sequence 40, Appl
1264	97	4.2	335	4	US-10-240-540-16	Sequence 16, App	1336	94	4.1	340	5	US-11-038-360-2	Sequence 117, App
1265	97	4.2	335	5	US-10-975-367-16	Sequence 16, Appl	1337	94	4.1	340	6	US-11-038-360-2	Sequence 2, Appl
1266	97	4.2	335	5	US-10-511-549-4	Sequence 4, Appl	1338	94	4.1	474	4	US-11-127-877-53	Sequence 53, Appl
1267	97	4.2	343	3	US-09-886-055-411	Sequence 411, App	1339	94	4.1	494	6	US-10-437-963-175542	Sequence 175542, App
1268	97	4.2	343	3	US-09-804-291-411	Sequence 411, App	1340	94	4.1	495	3	US-11-079-463-8915	Sequence 7, Appl
1269	97	4.2	343	4	US-10-343-650A-496	Sequence 496, App	1341	94	4.1	495	3	US-09-915-181A-7	Sequence 7, Appl
1270	97	4.2	343	4	US-10-467-252-13	Sequence 13, App	1342	94	4.1	495	4	US-10-755-889-588	Sequence 588, App
1271	97	4.2	343	5	US-10-819-316-411	Sequence 411, App	1343	94	4.1	495	5	US-10-823-506-2	Sequence 2, Appl
1272	97	4.2	428	6	US-11-087-099-10394	Sequence 10394, A	1344	94	4.1	495	5	US-10-631-467-768	Sequence 768, App
1273	97	4.2	528	6	US-11-097-143-24504	Sequence 24504, A	1345	94	4.1	518	4	US-10-104-047-3441	Sequence 3441, App
1274	97	4.2	540	5	US-10-732-923-22268	Sequence 22268, A	1346	94	4.1	518	6	US-11-072-512-3441	Sequence 2, Appl
1275	97	4.2	613	4	US-10-251-385-212	Sequence 212, App	1347	94	4.1	536	3	US-09-776-865-2	Sequence 8, Appl
1276	97	4.2	613	4	US-10-225-567A-356	Sequence 356, App	1348	94	4.1	536	5	US-10-823-506-8	Sequence 8, Appl
1277	97	4.2	663	3	US-09-781-880-5	Sequence 5, Appl	1349	93.5	4.0	569	4	US-10-282-122A-75619	Sequence 75619, A
1278	97	4.2	663	4	US-10-466-720-2	Sequence 2, Appl	1350	93.5	4.0	609	6	US-11-087-099-82855	Sequence 82855, App
1279	97	4.2	691	4	US-10-094-749-2607	Sequence 2607, App	1351	93.5	4.0	609	6	US-11-188-298-18635	Sequence 18635, A
1280	97	4.2	691	4	US-10-429-160-78	Sequence 78, App	1352	93.5	4.0	633	3	US-09-949-029-4	Sequence 4, Appl
1281	97	4.2	849	6	US-11-097-143-6303	Sequence 6303, App	1353	93.5	4.0	633	4	US-10-270-333-159	Sequence 159, App
1282	97	4.2	851	5	US-10-505-486-116	Sequence 116, App	1354	93.5	4.0	633	6	US-11-097-143-32514	Sequence 32514, A
1283	96.5	4.2	404	4	US-10-282-122A-67141	Sequence 67141, A	1355	93.5	4.0	649	4	US-10-282-122A-53761	Sequence 53761, A
1284	96.5	4.2	454	4	US-10-282-122A-70458	Sequence 70458, A	1356	93.5	4.0	865	6	US-11-188-298-17345	Sequence 17345, A
					US-10-724-972A-4461	Sequence 4461, App	1357	93.5	4.0	928	5	US-10-841-129-6	Sequence 6, Appl

1358	93.5	4.0	950	5	US-10-732-923-22431	Sequence 22431, A	1431	91	3.9	369	3	US-09-826-508-36	Sequence 36, Appl
1359	93	4.0	237	6	US-11-096-568A-19997	Sequence 19997, A	1432	91	3.9	369	5	US-10-149-826-7	Sequence 7, Appl
1360	93	4.0	241	6	US-11-096-568A-19996	Sequence 19996, A	1433	91	3.9	372	4	US-10-081-816-30	Sequence 30, Appl
1361	93	4.0	335	4	US-10-094-417-18	Sequence 18, Appl	1434	91	3.9	372	4	US-10-447-328-32	Sequence 32, Appl
1362	93	4.0	335	4	US-10-278-455-25	Sequence 25, Appl	1435	91	3.9	419	3	US-09-826-508-34	Sequence 34, Appl
1363	93	4.0	335	4	US-10-278-437-25	Sequence 25, Appl	1436	91	3.9	419	3	US-09-875-076-2	Sequence 2, Appl
1364	93	4.0	335	6	US-11-086-846-18	Sequence 18, Appl	1437	91	3.9	419	3	US-09-876-252-2	Sequence 2, Appl
1365	93	4.0	356	4	US-10-447-328-82	Sequence 82, Appl	1438	91	3.9	419	3	US-09-811-838-8	Sequence 8, Appl
1366	93	4.0	337	4	US-10-369-493-943	Sequence 943, App	1439	91	3.9	419	3	US-09-953-686-8	Sequence 8, Appl
1367	93	4.0	339	4	US-10-225-567A-360	Sequence 360, App	1440	91	3.9	419	4	US-10-225-567A-569	Sequence 569, App
1368	93	4.0	339	4	US-10-712-124-14	Sequence 14, Appl	1441	91	3.9	419	4	US-10-272-983-2	Sequence 2, Appl
1369	93	4.0	339	5	US-10-287-436A-579	Sequence 579, App	1442	91	3.9	419	4	US-10-275-703-1	Sequence 1, Appl
1370	93	4.0	339	6	US-11-152-366-45	Sequence 45, Appl	1443	91	3.9	419	4	US-10-393-807-2	Sequence 2, Appl
1371	93	4.0	454	6	US-11-087-099-11610	Sequence 11610, A	1444	91	3.9	419	4	US-10-417-820A-2	Sequence 2, Appl
1372	93	4.0	454	6	US-11-188-298-10739	Sequence 10739, A	1445	91	3.9	419	4	US-10-455-127-2	Sequence 2, Appl
1373	93	4.0	613	4	US-10-292-525-2	Sequence 2, Appl	1446	91	3.9	419	4	US-10-723-955-2	Sequence 2, Appl
1374	93	4.0	613	5	US-10-482-029-249	Sequence 249, App	1447	91	3.9	419	4	US-10-782-596-2	Sequence 2, Appl
1375	93	4.0	613	5	US-10-482-028C-2	Sequence 2, Appl	1448	91	3.9	419	5	US-10-684-206-18	Sequence 18, Appl
1376	92.5	4.0	296	6	US-11-188-298-16100	Sequence 16100, A	1449	91	3.9	419	5	US-10-723-955-2	Sequence 2, Appl
1377	92.5	4.0	354	6	US-11-096-568A-23661	Sequence 23661, A	1450	91	3.9	419	6	US-11-067-884-8	Sequence 8, Appl
1378	92.5	4.0	504	4	US-10-238-075-614	Sequence 614, App	1451	91	3.9	439	4	US-10-282-122A-74025	Sequence 74025, A
1379	92.5	4.0	591	4	US-10-282-122A-74312	Sequence 74312, A	1452	91	3.9	439	5	US-10-472-928-2710	Sequence 2710, App
1380	92.5	4.0	663	4	US-10-282-122A-59897	Sequence 59897, A	1453	91	3.9	500	4	US-10-282-122A-57785	Sequence 57785, A
1381	92.5	4.0	4226	5	US-10-732-923-22707	Sequence 22707, A	1454	91	3.9	512	4	US-10-335-977-5674	Sequence 5674, App
1382	92	4.0	349	3	US-09-966-782A-11	Sequence 11, Appl	1455	91	3.9	657	5	US-10-505-486-48	Sequence 48, Appl
1383	92	4.0	349	3	US-09-992-331-12	Sequence 12, Appl	1456	91	3.9	752	4	US-10-425-115-239772	Sequence 239772, A
1384	92	4.0	349	4	US-10-090-569-5	Sequence 5, Appl	1457	91	3.9	752	5	US-10-476-460-23	Sequence 23, Appl
1385	92	4.0	349	4	US-10-212-980-7	Sequence 7, Appl	1458	91	3.9	913	5	US-10-957-503-5	Sequence 5, Appl
1386	92	4.0	349	4	US-10-225-567A-126	Sequence 126, App	1459	91	3.9	2227	4	US-10-736-883-38	Sequence 38, Appl
1387	92	4.0	349	4	US-10-362-313-12	Sequence 12, Appl	1460	90.5	3.9	354	6	US-11-096-568A-15100	Sequence 15100, A
1388	92	4.0	349	4	US-10-166-568-2	Sequence 2, Appl	1461	90.5	3.9	355	4	US-10-251-385-2	Sequence 2, Appl
1389	92	4.0	349	4	US-10-254-905-11	Sequence 11, Appl	1462	90.5	3.9	355	4	US-10-225-567A-243	Sequence 243, App
1390	92	4.0	349	4	US-10-359-285-6	Sequence 6, Appl	1463	90.5	3.9	355	6	US-11-218-281-26	Sequence 26, Appl
1391	92	4.0	349	4	US-10-353-690-84	Sequence 84, Appl	1464	90.5	3.9	391	6	US-11-188-298-608	Sequence 608, App
1392	92	4.0	349	4	US-10-768-878-12	Sequence 12, Appl	1465	90.5	3.9	396	4	US-10-282-122A-50261	Sequence 50261, A
1393	92	4.0	349	6	US-11-060-291-17	Sequence 17, Appl	1466	90.5	3.9	407	6	US-11-188-298-22248	Sequence 22248, A
1394	92	4.0	350	6	US-11-079-463-7480	Sequence 7480, App	1467	90.5	3.9	442	4	US-10-335-977-5310	Sequence 5310, App
1395	92	4.0	413	4	US-10-474-776-235	Sequence 235, App	1468	90.5	3.9	445	3	US-09-799-978-34	Sequence 34, Appl
1396	92	4.0	413	5	US-10-472-928-544	Sequence 544, App	1469	90.5	3.9	445	4	US-10-649-853-34	Sequence 34, Appl
1397	92	4.0	446	4	US-10-299-642-32	Sequence 32, Appl	1470	90.5	3.9	446	4	US-10-282-122A-55022	Sequence 55022, A
1398	92	4.0	457	4	US-10-195-518-6	Sequence 6, Appl	1471	90.5	3.9	446	5	US-10-503-135-130	Sequence 130, App
1399	92	4.0	482	4	US-10-767-701-46532	Sequence 46532, A	1472	90.5	3.9	446	6	US-11-188-298-22502	Sequence 22502, A
1400	92	4.0	552	4	US-10-391-074-4	Sequence 4, Appl	1473	90.5	3.9	491	4	US-10-369-493-6372	Sequence 6372, App
1401	92	4.0	1027	4	US-10-125-792-2	Sequence 2, Appl	1474	90.5	3.9	497	6	US-11-188-298-4972	Sequence 4972, App
1402	92	4.0	1027	4	US-10-125-778-2	Sequence 2, Appl	1475	90.5	3.9	515	3	US-09-892-851-2	Sequence 2, Appl
1403	92	4.0	1027	4	US-10-268-051-8	Sequence 8, Appl	1476	90.5	3.9	515	5	US-10-897-019-2	Sequence 2, Appl
1404	92	4.0	1027	4	US-10-125-772-2	Sequence 2, Appl	1477	90.5	3.9	520	4	US-10-369-493-23311	Sequence 23311, A
1405	92	4.0	1027	4	US-10-410-885-2	Sequence 2, Appl	1478	90.5	3.9	520	6	US-11-087-099-7402	Sequence 7402, App
1406	92	4.0	1027	4	US-10-116-496-2	Sequence 2, Appl	1479	90.5	3.9	638	4	US-10-335-592-11	Sequence 11, Appl
1407	92	4.0	1027	5	US-10-851-047-8	Sequence 8, Appl	1480	90.5	3.9	706	5	US-10-501-282-2868	Sequence 2868, App
1408	92	4.0	1027	6	US-11-085-964-2	Sequence 2, Appl	1481	90.5	3.9	861	5	US-10-617-320-2860	Sequence 2860, App
1409	92	4.0	1027	6	US-11-086-550-2	Sequence 2, Appl	1482	90.5	3.9	1046	4	US-10-369-493-3073	Sequence 3073, App
1410	92	4.0	1037	6	US-11-086-832-2	Sequence 2, Appl	1483	90.5	3.9	4226	5	US-10-732-923-22586	Sequence 22586, A
1411	92	4.0	1037	6	US-11-079-463-6200	Sequence 6200, App	1484	90	3.9	324	3	US-09-800-321A-73	Sequence 73, Appl
1412	92	4.0	1170	4	US-10-208-731-6	Sequence 6, Appl	1485	90	3.9	324	4	US-10-305-555-11	Sequence 11, Appl
1413	92	4.0	2336	4	US-10-033-026-10	Sequence 10, Appl	1486	90	3.9	329	3	US-09-725-285-9	Sequence 9, Appl
1414	92	4.0	2336	4	US-10-736-883-30	Sequence 30, Appl	1487	90	3.9	329	3	US-09-195-662A-9	Sequence 9, Appl
1415	91.5	4.0	374	4	US-10-282-122A-63616	Sequence 63616, A	1488	90	3.9	329	3	US-09-339-912A-9	Sequence 9, Appl
1416	91.5	4.0	339	4	US-10-425-115-196274	Sequence 196274, A	1489	90	3.9	329	3	US-09-502-783A-9	Sequence 9, Appl
1417	91.5	4.0	415	4	US-10-425-114-62725	Sequence 62725, A	1490	90	3.9	329	4	US-10-791-905-9	Sequence 9, Appl
1418	91.5	4.0	463	3	US-09-738-626-6706	Sequence 6706, App	1491	90	3.9	329	5	US-10-127-764-9	Sequence 9, Appl
1419	91.5	4.0	463	4	US-10-627-476-630	Sequence 630, App	1492	90	3.9	332	6	US-11-188-298-19569	Sequence 19569, A
1420	91.5	4.0	488	6	US-11-188-298-16632	Sequence 16632, A	1493	90	3.9	349	3	US-09-826-509-503	Sequence 503, App
1421	91.5	4.0	488	4	US-10-017-161-742	Sequence 742, App	1494	90	3.9	349	5	US-10-925-095-503	Sequence 503, App
1422	91.5	4.0	503	6	US-10-032-585-7822	Sequence 7822, App	1495	90	3.9	366	4	US-10-017-161-2098	Sequence 2098, App
1423	91.5	4.0	762	6	US-11-188-298-11787	Sequence 11787, A	1496	90	3.9	366	4	US-10-292-798-1744	Sequence 1744, App
1424	91.5	4.0	821	6	US-11-188-298-3481	Sequence 3481, App	1497	90	3.9	478	6	US-10-276-774-2085	Sequence 2085, App
1425	91.5	4.0	850	4	US-10-474-776-421	Sequence 421, App	1498	90	3.9	478	6	US-11-096-568A-30175	Sequence 30175, A
1426	91.5	4.0	850	5	US-10-472-928-4682	Sequence 4682, App	1499	90	3.9	505	4	US-10-156-761-11827	Sequence 11827, A
1427	91.5	4.0	926	3	US-09-816-685-2	Sequence 2, Appl	1500	90	3.9	514	6	US-11-096-568A-30174	Sequence 30174, A
1428	91.5	4.0	926	4	US-10-639-708-2	Sequence 2, Appl							
1429	91.5	4.0	1896	5	US-10-732-923-1758	Sequence 1758, App							
1430	91	3.9	225	5	US-10-472-928-88	Sequence 88, Appl							

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GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on: June 6, 2006, 21:58:15 ; Search time 41 Seconds
(without alignments)
1044.304 Million cell updates/sec

Title: US-10-063-537-32
Perfect score: 2315
Sequence: 1 MSGRDITLGLIALALSLA.....QQDKSLRNEEGTELOAIVR 445

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	505	21.8	771	2 T16254	hypothetical prote
2	257.5	11.1	523	2 T05692	hypothetical prote
3	179	7.7	488	2 C86385	hypothetical prote
4	177.5	7.7	574	2 T41068	hypothetical prote
5	163	7.0	539	2 S67049	probable membrane
6	126	5.4	372	2 S52054	ubiquinol-cytochro
7	119	5.1	523	2 T11916	NADH2 dehydrogenas
8	118.5	5.1	619	2 T11314	NADH2 dehydrogenas
9	118	5.1	497	1 S53834	NADH2 dehydrogenas
10	117.5	5.1	338	2 S50339	NADH2 dehydrogenas
11	115	5.0	868	2 E89897	conserved hypothet
12	113	4.9	633	2 G95385	Kup2 Potassium upt
13	111	4.8	493	2 S78183	NADH2 dehydrogenas
14	110.5	4.8	694	2 E69143	hypothetical prote
15	110	4.8	495	1 S25942	NADH2 dehydrogenas
16	109	4.7	501	2 B71707	ADP,ATP carrier pr
17	108.5	4.7	608	2 C70111	V-type ATPase, sub
18	108	4.7	474	2 B64232	hypothetical prote
19	108	4.7	1783	2 T37258	probable voltage-d
20	108	4.7	1917	2 C88728	protein C48A7.1 [i
21	107.5	4.6	447	2 AG0377	probable O-unit fl
22	107.5	4.6	627	2 D90452	hypothetical prote
23	107.5	4.6	763	2 T48702	hypothetical prote
24	106.5	4.6	501	2 B97790	ADP,ATP carrier pr
25	106.5	4.6	694	2 T13572	NADH2 dehydrogenas
26	106	4.6	495	2 T12401	NADH2 dehydrogenas
27	106	4.6	497	1 WNBELM	membrane protein L
28	106	4.6	503	2 D70930	hypothetical prote
29	106	4.6	677	2 T50022	sulfate transporte

30	105.5	4.6	332	2 B82876	oligopeptide trans
31	105	4.5	782	2 T25925	hypothetical prote
32	104.5	4.5	342	2 T29245	hypothetical prote
33	104.5	4.5	475	2 S73746	MG294 homolog A05
34	104.5	4.5	492	2 E58931	NADH2 dehydrogenas
35	104	4.5	245	2 B60944	ubiquinol-cytochro
36	104	4.5	445	2 E22845	hypothetical prote
37	104	4.5	544	2 C96943	uncharacterized me
38	103.5	4.5	250	2 C60944	ubiquinol-cytochro
39	103	4.4	446	2 S01187	NADH2 dehydrogenas
40	103	4.4	461	2 S60253	sel-12 protein - C
41	103	4.4	518	2 A53207	probable folate tr
42	103	4.4	602	2 D90557	hypothetical prote
43	103	4.4	1128	2 T04922	hypothetical prote
44	102.5	4.4	306	2 A33960	cytochrome caa3 ox
45	102	4.4	383	2 S55594	G protein-coupled

ALIGNMENTS

RESULT 1

T16254
hypothetical protein F35C8.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16254
R;Wu, X.

submitted to the EMBL Data Library, November 1995
A;Description: The sequence of C. elegans cosmid F35C8.
A;Reference number: Z18486
A;Accession: T16254
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-771 <WUX>
A;Cross-references: UNIPROT:Q20026; UNIPARC:UPI000007C755; EMBL:U40941; NID:gi072184; PIR
C;Genetics:
A;Gene: CESP:F35C8.7
A;Introns: 87/2; 143/2; 238/1; 289/2; 428/2; 629/3; 678/1; 712/1; 736/1

Query Match	21.8%	Score	505;	DB 2;	Length	771;			
Best Local Similarity	28.9%	Pred. No.	5.4e-34;						
Matches	131;	Conservative	95;	Mismatches	180;	Indels	48;	Gaps	13;
Qy	10	LCILALALS	LAMMFTFRFTTLLVHIFISLVILGLLFVCGVLW--WLYDYDT---NDLSI	64					
Db	318	LIFAAGILSFIVTMRLGSLIILVILVALGFGAGFSMLKNTLTATTCAIDDDYSF	377						
Qy	65	E--LDTERENMKCVLGFVAIVSTGITAIVLVILFVLRKRIKLTVELFQITNKAISSAPFL	122						
Db	378	HPAFDAYFEMPTTTLVVAIATSVLLIFLLVILFIQIRISIAICALISESSKALIGSMWSTL	437						
Qy	123	FQPLWTFAILIFPWLWVAVLLSLGTAG--AAQVME--GGQVEYK-----PLSGIRY	170						
Db	438	LPFLFPFLLHIGVFWALGWSIAIWLASSGQEVCKLTNGQV-YNTSTKCDCTAKVTGCTY	496						
Qy	171	M-----W---SYHLIGLIWTSFFILACQOMTIAGAVVTTCYFNRSK-NDPPDHPILS	217						
Db	497	VGIEKSEITFWLVQVYNLFAFFWLSCFVTALGDIALAGAPASYYWARDKRDVPTFPVIR	556						
Qy	218	SLSILFFYHQGTIVKGSFLISVVRIPRIIVMYNQNALKEOQHGALSRYLPRCCVCCFWCL	277						
Db	557	ALNRAIRYNLGSIFAGSLIIAIVKIIRVLEIDHKLKGSQNKAVKWFML-CLKKCCFWCL	615						
Qy	278	DKVLLHLNQAYTTTAINGTDFCTSAKDAFKILSKSSSHFTSINCFDGFIFLQKVLVVC	337						
Db	616	EVFFKFLTKNAYIMAIYGNPFSSAKDSFLLIRNIVRTVVVHKVAGILFLFKGSMI--	673						
Qy	338	FTVFGGLMAFNYNRAQV-----WAVPLLVAFAYLVAHLSFLSVFETVLDAFL	386						
Db	674	-TLGMSGLISFYFSGRWVVEGVPKVDLYYFVPDIVIVIGSVYFMADLFFDVIYEMAVDTTF	732						
Qy	387	LCPAVDLETNDGSEKPYRWDQEFLLFVFKRSNKL	420						

Db 733 ICFLDESEQNGSLERPPFFMSEKLLLEILGNKNDI 766

RESULT 2
T05692
hypothetical protein F20M13.200 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05692
R;Revan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.
submitted to the Protein Sequence Database, February 1999
A;Reference number: Z15420
A;Accession: T05692
A;Molecule type: DNA
A;Residues: 1-523 <BEV>
A;Cross-references: UNIPROT:Q9S2P2; UNIPARC:UPI000000A31F2; EMBL:AL035540
A;Experimental source: Cultivar Columbia; BAC clone F20M13
C;Genetics:
A;Map position: 4
A;Introns: 264/2; 339/2; 391/3; 437/3
A;Note: F20M13.200

Query Match 11.1%; Score 257.5; DB 2; Length 523;
Best Local Similarity 24.6%; Pred. No. 1.2e-13;
Matches 100; Conservative 75; Mismatches 160; Indels 71; Gaps 16;

QY 6 TILGCLALALSLAMWTFRTITLLVHIFISLVILGLLFVCGVLMWLYDYDNDLSIE 65
Db 145 TLVVTLLSVPFCFVLLLLKHVTQIVACLPFLVLPPIFF-NVYWFVACTLSSCSDA 203

QY 66 LDTRENMKCYLGFALVSTGITAIVLLVIFVLKRIKLTVELFQITNKALISSAPFLLPQ 125
Db 204 LPLAYRILVLFVFLII-----GIIVHIIIVANWHRIDLTQIISVASDALS-----KN 251

QY 126 LMTFAILIFPWLWVAIVSLGTAGAAQVME-GGQ--VEYKPLSGIRYMWSYHLIGLIWT 182
Db 252 LKLFVVL-----PLLTLGFNGKVPRELQGVCEWKEKSDWPAYYALAILTWS 302

QY 183 SEFILACQOMTIAGAVVTCYFNRSKNDP--PDHPILSLSLFFYHQTGVVKGSLISVVR 241
Db 303 LAVVENQVYVVISGAIQAQWYF--SKEDSIPKCIIRSLRNAFQGSFGTICVSGLLICIVR 360

QY 242 IPRILVYMQNALKEOQHAGLSRYLPRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCT 301
Db 361 VVRAIV--DNAREBNTQGIWNVML-RCC-----ANALLGEAYCT 396

QY 302 SAKDAFKILSKN--SSHF-----TSINCFGDFIIFLGKVLVWCFTVFGGLMAF--NYNR 351
Db 397 SAKWTYELLRLNLSAVFVETVSTRI-LTGIVFVLSAAYAVATWAVLRGVSNLGDYSYV 455

QY 352 AFQWNAVPLLLVAFFAYLVAHSFLSVFETVLDALFLCFAVDLETND 397
Db 456 AVLAWVLLIVILAFVH-----VLDDVIDTIYVCYAI DRDKGD 493

RESULT 3
T05692
hypothetical protein F20J7.7 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C86385
R;Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizlar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Accession: C86385
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-488 <STO>
A;Cross-references: UNIPROT:Q9C6L9; UNIPARC:UPI000000A87B5; GB:AE005172; NID:gl0092332; PJ
C;Genetics:
A;Map position: 1

Query Match 7.7%; Score 179; DB 2; Length 488;
Best Local Similarity 21.1%; Pred. No. 3.6e-07;
Matches 85; Conservative 62; Mismatches 146; Indels 110; Gaps 18;

QY 21 MMFTFRFITLLVHIFISLVILGLLFVCGVLMWLYDYDNDLSIELDTERENMKCYLGFA 80
Db 128 MKVSVHILTYLA-----VVSVLCFWCRLFFW-----GGA 157

QY 81 IVSTGTAVLLVL-----IFVLRKRIKLTVELFQITNKALISSAPFLLPQPLWTFAL 131
Db 158 FAVGSLLOFLYVISVIDRLPFTMLVLRKALKLVWGLPKVIMVA-----HAFTV 205

QY 132 LIFFVW-LAWAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFTLACQ 190
Db 206 VMLLMWLSLW-----SFGAAGVWASSMGDE-----GRWLLVVLVSFLWTCGAVLCNTV 253

QY 191 QMTIAGAVVTCYFNRSKNDP--PDHPILSLSLFFYHQTGVVKGSLISVVRIPRIIV 247
Db 254 HVIIVGSMVPHVLFHCQEESSSLPSSSLVDSLRYAVTTSGFSICYGSLFTAAIR----- 307

QY 248 MYMQNALKEOQHAGLSRYLPRCCYCCFWCLDKYLLHL-----NONAYTTTAINGTDF 299
Db 308 -----TLRWEIRGFRSKICGNECLLC--CVD-FLFHLVETLVRFFNKYAYVQIAVYKGF 359

QY 300 CTSAKDAFKIL-SKNSHETSINCEGDFIIFLGKVLVWCFTVFGGLMAFNRYNRAFOVWA- 357
Db 360 NKSARDAWELFPOSTGVLEALVAYDCSG-AVLLMG-----TIFGGIIT---GSCIGINAW 408

QY 358 ----VPLLVAFAVYLAHVSFLS-----VFETVLDALFLCFAVD 392
Db 409 IKYSDRVINVA STM LMGVNLGVMVVS AVTSIYICFAED 451

RESULT 4
T41068
hypothetical protein SPCC1682.11c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T41068
R;Murphy, L.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z21968
A;Accession: T41068
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-574 <MUR>
A;Cross-references: UNIPROT:O74441; UNIPARC:UPI0000006ABD2; EMBL:AL031525; PIDN:CAA20677.1
A;Experimental source: strain 972h; cosmid c1682
C;Genetics:
A;Gene: SPDB:SPCC1682.11c
A;Map position: 3
A;Introns: 5/1; 358/2; 538/2
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPCC1682.11c

Query Match 7.7%; Score 177.5; DB 2; Length 574;
Best Local Similarity 21.4%; Pred. No. 5.7e-07;
Matches 91; Conservative 76; Mismatches 159; Indels 99; Gaps 20;

QY 12 ILALALSLAMWTFRTITLLVHIFISLVILGLLFVCGVLMWLYDYDNDLSIELDTERE 71
Db 192 IICMMLSVIIVLFCVLVAIPRFLYFLLASVPLTMTFAFAYLL-----KASRIHLETSIQ 243

QY 72 NMKCVLGFPAIVSTGI---TAVLLVILFVLKRI--KLTVELFQITNKALISSAP-----EL 121
Db 244 PKLMELI-----TGIILLVAPILLSYVWRRRIHFHFTSFNIRKLACRVADIPOITLIFI 297

```

QY      122 LFQPLWTFAILLFFWLVAVULLSLGT--AGAAQWMEGQVETKPLSGIRYMW-----SYHL 176
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      298 SF--LFSPFYLFIVWRLFARFLRGSTLVGSMVVL P-----RSSWVLASFYS 343
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      177 IGLIWTSEFILAQQMTIAGAVVTCYENRKNKDPDPHPILSSILSILFFVH-----QGTVV 231
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      344 LHFLMLCTFFHALQCAIISSIVSQWFFYR---DTKSSATKTNLVSHFFVHVVSNOYGLCA 400
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      232 KGSPLISVVRIPRIITVMYMONALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNYTT 291
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      401 FSSPLVWITKVP---LHFLPTWL-----RHVSRIVY-----YMFSEKTSASYVT 440
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      292 T-----AINGTDCTCAKDAFKI-----LSKNSSHFTSINCFGDPIIFLGKVLVVC 337
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      441 SPLTLAYASIVSPYMNASKALYQIEQLNRVGLRRRSYFSK-----YTLAARSL-- 492
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY      338 FTVFGLMAFNY---NRAFOVWAPLLLVAFPAVLVAHSPUSVPETVLDALFLCFADVLD 393
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      493 -AIGVGVTSWNYSHENGVFYGYIVG--LLGGFLAWLIIGAIEGGLSMIVDALLICSIIDI 550
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QY      394 ETNDG 398
      |
Db      551 SSCQG 555

RESULT 5
S67049
probable membrane protein YOR161c - Yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein O3568
C:Species: Saccharomyces cerevisiae
C:Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
C:Accession: S67049
R:Bordonne, R.; Camasses, A.; Madania, A.; Martin, R.P.; Poch, O.; Tarassov, I.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S67032
A:Accession: S67049
A:Molecule type: DNA
A:Residues: 1-539 <BOR>
A:Cross-references: UNIPROT:Q12412; UNIPARC:UPI0000069D51; EMBL:Z75069; NID:gl
A:Experimental source: strain S288C

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Query Match 5.4%; Score 126; DB 2; Length 372;
Best Local Similarity 20.7%; Pred. No. 0.0069;
Matches 92; Conservative 64; Mismatches 124; Indels 164; Gaps 24;

Qy 10 LCIALALSLAMMTFFRITLLVHIFISLVILGLFVCGLWMLYYD-----YTND 61
Db 17 LCCULLSGDLFRVYGLGNLGVMIQLI-----LVGIC--LSWFFRCIIQNWIFTLL 68
Qy 62 LSIELDERENMKCVLGAIVSTGI--TAVILLVLFLVKRIKLTVELFQITNKAISSAP 119
Db 69 IHLEFD-----LGPIIRSLHIPTSLYFLAYIHKIIFLCILFDSS----- 111
Qy 120 FLFPQPLWTFAILLFFVWLVAVLLSLG-TAGAAOMEGGQVEYK-----PLSGIRYMW 172
Db 112 ---MLVMFGFLIFILIIAF---IGYTLPTCSMYMGLTVFSNILATIPLIGI---- 160
Qy 173 SYHLIGLITSEFI-----LACQOMTIAGA--VVTCTYFNRSKNDDPPDPHIL 216
Db 161 --YTCQMWCSEFINDFTLKLHSIHIFLPVLLFLIGAHHFVLYHYF-----L 206
Qy 217 SSSLIL-----FFVHQGTQVWKVGSFLISVVRIPIIVMYMQNALKEQHGLSRYLF 267
Db 207 SSDGLLDORPPPYERFFFLLYLRLDELFI--INTLCFLIYI----- 247
Qy 268 RCYCPCWCWLDKYLLHLNLNQNAYYTTTAINGTD-----FCTSANDAFKILSKNS 314

164 PLSGIR----YMSYHLIGLITSEFILACQOMTIAGAVVTCYF-NRSKNDDPPHPILSSL 219
Db 276 KLIGLVVVVFPGYYI-----SEVRNVHCVISGVFGSWYMSKSDQGMWRPWFALG 329
Qy 220 SILPFYHOGTVVKGSLISVVRIPRIIVMYMNALKQQHGALSRYLFCYCCF-WCLD 278
Db 330 KRAMTYSFGSCFSGLLVALIDLLOLMIRHDVTSSGGQIA---IQILFMVFDWIIG 386
Qy 279 --KYL-HLNQNAVTTTTAINGPDFCTSAKDAPFKILSKN-----SSHFTSI-----NCFG 324
Db 387 FLKWLAEYNHVAYSFYALYGPKYLRRAKETWMYMLREKMGMDALINDNLINIALGLFSMPA 446
Qy 325 DFIFELGKVLVVCFT-----VFGGLMAFNYNRAFQW-----AVPLLVAFFAYL- 369
Db 447 SYMTALFTFLYLRFTSPQYNSNGAYNGALMAFSFVIALQICNIATEAIRSGTATTFVALG 506
Qy 370 -----VAHSFLSVFETVLDAL 385
Db 507 NDPEVFHSHYPHRDEIFRAYPDVL 531

RESULT 6
S52054
ubiquinol-cytochrome-c reductase (EC 1.10.2.2) cytochrome b - Trypanoplasma borreli mito
C/Species: mitochondrion Trypanoplasma borreli
C/Date: 14-Jul-1995 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C/Accession: S52054
R/Lukes, J.; Arts, G.J.; van den Burg, J.; de Haan, A.; Opperdoes, F.; Sloof, P.; Benne,
EMBO J. 13, 5086-5098, 1994
A>Title: Novel pattern of editing regions in mitochondrial transcripts of the cryptobid
A/Reference number: S52053; MUID:95045401; PMID:7525275
A/Accession: S52054
A/Molecule type: mRNA
A/Residues: 1-372 <LUK>
A/Cross-references: UNIPROT:Q33568; UNIPARC:UPI0000128B2E; EMBL:U11684; NID:G563141; PID:
C/Genetics:
A/Gene: cyt b
A/Genome: mitochondrion
A/Genetic code: SGC6
C/Superfamily: cytochrome b; cytochrome b homology; cytochrome b6 homology; plastoquinol.
C/Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; mitochondrion;
F/10-343/Domain: cytochrome b homology <CBH>
F/10-211/Domain: cytochrome b6 homology <CB6>
F/225-343/Domain: plastoquinol-plastocyanin reductase 17K protein homology <17K>
F/83,184/Binding site: heme iron (His) (axial ligands) (low potential) #status predicted
F/97,198/Binding site: heme iron (His) (axial ligands) (high potential) #status predicted

```
Db 248 ----CIYW-----FPFHESWIIIVDTLTKSDKILPEWFFLSFFGFLKSVDPKF----- 292
QY 315 SHETSINCFGDFIIFLGKVLVVCFTVF-----GGMAFNYNRAFOVWAVPLLLVAFAYLV 370
Db 293 -----MGLFLULF-----VLCFAFLFILNCILFIYCRSLLW-MSLSULIFY-YLC 337
QY 371 AHSFLSVFETVLDALFCFAVDLE 394
Db 338 VGCFLSLY-----VVLCPFLLWWE 355

RESULT 7
T11916
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Prototheca wickerhamii mitochondrion
C;Species: mitochondrion Prototheca wickerhamii
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T11916
R;Wolff, G.; Plante, I.; Lang, B.F.; Kueck, U.; Burger, G.
J. Mol. Biol. 237, 75-86, 1994
A;Title: Complete sequence of the mitochondrial DNA of the chlorophyte alga Prototheca wickerhamii
A;Reference number: Z17373; MUID:94180393; PMID:8133522
A;Accession: T11916
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-523 <WOL>
A;Cross-references: UNIPROT:Q37617; UNIPARC:UPI0000130787; EMBL:U02970; NID:g467843; PID:11916
A;Experimental source: strain HB-8
C;Genetics:
A;Genome: mitochondrion
A;Note: nad4
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 5.1%; Score 119; DB 2; Length 523;
Best Local Similarity 18.1%; Pred. No. 0.037;
Matches 76; Conservative 63; Mismatches 163; Indels 118; Gaps 15;

QY 11 CILALALSAMMFTFRITLLVHIFISVLILGLLFCVGLWMLVYDYNLSIELDTER 70
Db 151 CIAFLVETLMLTVFSLVDLLFIIFPESVLIPWFIIGV-WG-----SRER 196
QY 71 ENMKCVLGAIVTGTAVALLVFLVRKRIKLTVELFQITNKAISSAPFLLPQMLTFA 130
Db 197 KIRAAQFFLYTLFGSVLMLAIIILYFQGTLDIEMLYLSDSETRQCILWLAFASFA 256
QY 131 IL-----IPFW-----VLWAVLLSIGTAG-----AAQWEGGVQVYKPLSGI 168
Db 257 VKVPMVPVHIWLPFAHVEAPTAGSVILAGILLKLTGYGLRFSIPLFPVACIYFTPL--- 313
QY 169 RYMWSYHLIGLIWTS-----EFLACQOMTIAGAVVTCYFNRSKNDPPDHPILSSL 219
Db 314 --IYTWSVIAIVTSCTHRIQDLKIIAYSSVAHNMNFVTIGLSQNT----- 359
QY 220 SILFFYHQGVWKGSLISVVVRIPIRIYVMQNALKEQHGALSRYLFRCCYCCFWCLDK 279
Db 360 -----QG---IGSILMT-----SHGLVSPALFLCVGLVY----- 387
QY 280 YLLHLNQNAVTTAINGTDFTCSAKDAFKILSKNSHFTSINCF-----GDFIIFLG 331
Db 388 -----DRHKRLRLRYSGCGTMTPIFALL---FVFFTMANISLPQTSFPGFEFLVFIG 437
QY 332 KVLVVCFTVPGGLMAFNYNRAFOVWAVPLLLVAFAYLVNAH-SFLSVFETVLDALFCFA 390
Db 438 SYQNNSFVAFCAATGMVLGAAYALMLCNRLI-----YGVSKPDFINTWSDNRRFFMFA 492

RESULT 8
T11314
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Pedinomonas minor mitochondrion
C;Species: mitochondrion Pedinomonas minor
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T11314
R;Turmel, M.; Lemieux, C.; Burger, G.; Lang, B.F.; Otis, C.; Plante, I.; Gray, M.W.
```

```
submitted to the EMBL Data Library, December 1998
A;Description: The complete mitochondrial DNA sequences of Nephroselmis olivacea and Pedicellina
A;Reference number: Z17261
A;Accession: T11314
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-619 <TUR>
A;Cross-references: UNIPROT:Q9ZY28; UNIPARC:UPI000008C2A6; EMBL:AF116775; NID:g4378766; I
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC3
A;Note: nad5
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 5.1%; Score 118.5; DB 2; Length 619;
Best Local Similarity 22.0%; Pred. No. 0.048;
Matches 105; Conservative 73; Mismatches 160; Indels 139; Gaps 24;

QY 7 ILGLCITLALALSAMMFTFRFITL-LLVHIFIS-----LVLILG 43
Db 124 ILVLVSENALTULFGWEGIGITSYLLINFWISKLOSGKSAKAVFLNRIGDSFFIALG 183
QY 44 LLFVCGVLWMLYDYDYNL-----SIELDTERENMK-CVLGFAIVSTGITAVLLVLIFVLR 98
Db 184 LTF-----YLFSGDDLFLISSLSVFYEKQIVKYLLIAYLIASTAKSAQILLHW-LP 234
QY 99 KRILKTVELFQITNKA--ISSAPFLLPQMLTFAILFF-----WVLWAVLISL--GTAG 150
Db 235 DAIEAPTIVSSLLHAATLVGAGVYLLIK--LSFLSLDDSSNFIIVGILTSFLAGLIG 292
QY 151 AAQWEGGVQVYKPLSGIRYMWSYHLIGLI-----WTSEFILLACQOMTIAGAVVTCY 202
Db 293 FNOPTDKRIIAVSTCSQIGLM--FYAIGLISLDFSVLHVFHGVFKLMLFAGAFIHI 350
QY 203 FNRSKNDPPDHP-----ILSSLSIL-PFYHQGTIVKVGSLISVVRIPIIWM 248
Db 351 FN--EQDIRKGYSLNFLNSFLSLAFVLSNLGLGIFFIAGFYSKELLISGI----- 400
QY 249 YMQNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVTTAINGTDFTCSAKDAFK 308
Db 401 YNN-----FWSL-----LSVLAIFTTCLYG-----IKSILL 427
QY 309 IL--SKNSHFTSINCFGD--FTIFLGKVLVVCFTVFG-----GLMAFNYNRAFOVWA 357
Db 428 VLSGSPWNSPFSITTYDNLVILSVLVLNFFFGPMITEQIKLMDIVYNS----- 482
QY 358 VPILLVAFAYLVNAHSFLSVFETVLDALFCFAVDLETNDGSSSEKPYFMDQBELSPV 414
Db 483 -----VFFS---IKSNLFLFEHVYVNWILFVISVFLILSNWYSIFFFSKLSLFI 530

RESULT 9
S53834
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Acanthamoeba castellanii mitochondrion
C;Species: mitochondrion Acanthamoeba castellanii
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S53834
R;Burger, G.; Plante, I.; Lonergan, K.M.; Gray, M.W.
J. Mol. Biol. 245, 522-537, 1995
A;Title: The mitochondrial DNA of the amoeboid protozoan, Acanthamoeba castellanii: comp
A;Reference number: S53825; MUID:95147275; PMID:7844823
A;Accession: S53834
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-497 <BUR>
A;Cross-references: UNIPROT:Q37375; UNIPARC:UPI000013072D; GB:U12386; NID:g562028; PIDN:
A;Experimental source: strain Neff; ATCC 30010
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C;Genetics:
A;Genome: mitochondrion
A;Genetic code: SGC6
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
```


Db 504 NSPFIYHNGISLYSIFNGDILKYDKTLQI 535

RESULT 12

G95385
Kup2 Potassium uptake protein [imported] - Sinorhizobium meliloti (strain 1021) magaplas
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: G95385
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bows
; Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C.
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti
A;Reference number: A95262; MUID:21396509; PMID:11481432
A;Accession: G95385
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-633 <KUR>
A;Cross-references: UNIPROT:Q92Y93; UNIPARC:UPI00000D4778; GB:AE006469; PIDN:AAK65649.1;
A;Experimental source: Strain 1021, megaplasmid pSymA
R;Galibert, F.; Finan, T.M.; Long, S.R.; Fuller, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
peia, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, B.; Komp, C.; Lelaure,
hebaull, P.; Vandenbol, M.; Vorholter, E.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: kup2
A;Genome: plasmid

Query Match 4.9%; Score 113; DB 2; Length 633;

Best Local Similarity 22.0%; Pred. No. 0.14;
Matches 49; Conservative 39; Mismatches 67; Indels 68; Gaps 9;

QY 3 GRDTILGLCTIALALSAMMFFRFTITLL-----VHIFISVILG-----LLFV 47
DB 54 GRDEVGLVSLV-WTLTAIVTIKYVFLLRANDGEGGTLGLALLKKGTQKYPVLMFF 112
QY 48 CGVLMWLY-----DYTNDSIELDTERENMKCVLGFVSTG-----ITAVLLVLFV 96
DB 113 AGVLAALFGDAMIPLSV-----LSAVEGLKVAPALHDYVLPISVVIIALLFA 164
QY 97 LRKRIKLTVELFOITNKAISSAPFLFQPLWTPAILIFFWLWVALLSLGTAGAQMWE 156
DB 165 VQSR-----GTGAUVFFGPIITLVWFLWMAAGVAHIGD 198
QY 157 GGQV--EYKPLSGIRYMWVHLGLIWTSEFILACQOMTIAGA 197
DB 199 DLALSAFNPNAIGFLWNAAGLIGFI-----VLGAIFLVTGA 236

RESULT 13

S78183
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Reclinomonas americana (ATCC 503
C;Species: mitochondrion Reclinomonas americana
A;Variety: ATCC 50394
C;Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 09-Jul-2004
C;Accession: S78183
R;Lang, B.F.; Burger, G.; O'Kelly, C.J.; Cedergren, R.; Golding, G.B.; Lemieux, C.; Sank
Nature 387, 493-497, 1997
A;Title: An ancestral mitochondrial DNA resembling a eubacterial genome in miniature.
A;Reference number: S78127; MUID:97311393; PMID:9168110
A;Accession: S78183
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-493 <LAN>
A;Cross-references: UNIPROT:O21286; UNIPARC:UPI000008D0BD; EMBL:AF007261; NID:G2258325;
A;Experimental source: ATCC 50394
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1997
C;Genetics:

A;Gene: nad4

A;Genome: mitochondrion

C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 4.8%; Score 111; DB 2; Length 493;

Best Local Similarity 21.8%; Pred. No. 0.16;

Matches 85; Conservative 53; Mismatches 128; Indels 124; Gaps 21;

QY 10 LCILALALSAMMFFRFTITLLVHIFISVILGGLFVCGVLWVLYDYDTNLSIELDTE 69
DB 120 ICFLLLDALLIMTFC--VLDLVLFIYFFSVLPIMPVIGV-WG-----SRE 163

QY 70 RENMKCVLGFVAVSTGITAVLVLIVL-----RKRIKLTVELFOITNKAISSAPFL 122
DB 164 RKVRAAYMLFLTYTFFG-SLMLAIAMVIYFDAGTTDQVLLTTEFSQERQKLWLAF 222

QY 123 FQ---PLMTFAILIFFW-----VLWVAVLLSLGTAG-----AAQVMEGQVVE 162
DB 223 FAIKIPMVFFHV---WLPEAHVEAPTAGSVLLAGVLLKGGVILRFSIPMPPEATVVF 278

QY 163 KPLSGIRYMWVHLGLIWTSEFILACQOMTIAGAVVTCYFNRSKNDDPDHPILSL 222
DB 279 TPL-----VYTMSSIIAIYTS--LTLRQIDLKRIIA-----YSSVA-- 313

QY 223 FFVHQGTVVKGSFLISVVRIPRIIVVMQNALKEQHQGALSRYLPRCCYCCFWCLDKY-- 280
DB 314 ---HMNFVTIGFSLNMQGLEGSILML-----SHGIVSSALFLCIGVLY--DRHKT 360

QY 281 -LIHLNQNAYTTTAINGTDFC--TSAKDAFKILSKNSHFTSINCFDGFIIIFLGKLVVVC 337
DB 361 RLLKYYSGVVQIMPFIATLFLMLFTMA---NISLPGTSSEFV-----GEPLVLIG----- 405

QY 338 FTVFGGLMAFNVRAPQVWAVPPLLVAFFA 367

DB 406 -----AFNSNTT-----VAFPA 417

RESULT 14

E69143

hypothetical protein MTH339 - Methanobacterium thermoautotrophicum (strain Delta H)
C;Species: Methanobacterium thermoautotrophicum
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: E69143

R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicare, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.;
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997

A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functi

A;Reference number: A69000; MUID:98037514; PMID:9371463

A;Accession: E69143

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-694 <MTH>

A;Cross-references: UNIPROT:O26439; UNIPARC:UPI0000062CSF; GB:AE000818; GB:AE000666; NID:

A;Experimental source: strain Delta H

C;Genetics:

A;Gene: MTH339

Query Match 4.8%; Score 110.5; DB 2; Length 694;

Best Local Similarity 20.5%; Pred. No. 0.25;

Matches 88; Conservative 73; Mismatches 164; Indels 105; Gaps 20;

QY 12 ILALALSAMMFFRFTITLLVHIFISVILV-----LGLLFVCGVLWVLY----- 56
DB 58 VIAAALSIFM---MMTGLIINSFPLMRPLSLPILSAINLLII--ALMVHYLHGE 111

QY 57 -----DYTNDSIELDTERENMKCVLGFVAVS--TGITAVLLVLIIFVLRKRKLTVELFQ 109
DB 112 EPLNLKASGNLSTALSSILFPVLTIVGSLYMKYSVNTVLLVLLF-----IPVYILLE 166

QY 110 ITNKAISSAPFLFQPLWTPAILIFFWVLMWVAVLSLGTAGAAQVMEGQVYKPLSGIR 169


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Db 167 VFKKKIQPA-----TYPVAIF-----SISLSL-----LIMGLPSNY--LIGRD 203
Qy 170 YMSYHILIGL-----IWTSEFILACQOMTIAGAVVTCYFNRSKNPDHPILSSL 219
Db 204 IHMEFYLFRRKALMAHMDHMGVSYNAYNACLSVTPLVPIYKVLN-----VPEV 252
Qy 220 SILFFYHQGTVMKGSFLISVVRIPRIIWMYMONALKEQHGALSRYL-----FRCYCFCW 275
Db 253 YIEKFYY-----GFIGALMPLP--VYLISERILKRSYGFYATLLFIQFSFIYILGW 303
Qy 276 CLDKYLHLNQNAYTTTAINGTDECTSAKDAFKILSKNS--SHFTSINCDFDFTIPLGKV 333
Db 304 C--RQLVALLFFAAAVMVLGDMRSHKLLFVFMVGTVLVSHVTTAYVF-----FFLVAL 357
Qy 334 LVVCFTVFGGLMAFNYNRAF--QVMVAPLLLVAFAYLVA-----HSFLSVFETVLDAIF 386
Db 358 IPILVRVMKRLKVPDDSKGFFAASLAVLFFVVFVAFWATGAPFKSAVSFFTTKLRSMS 417
Qy 387 LCFADVLETN 396
Db 418 EFFSADMRNN 427

RESULT 15
S25942
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - liverwort (Marchantia polymorpha)
N;Alternate names: NADH-ubiquinone oxidoreductase chain 4
C;Species: mitochondrion Marchantia polymorpha
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S25942; S31172
R;Oda, K.; Yamato, K.; Ohta, E.; Nakamura, Y.; Takemura, M.; Nozato, N.; Akashi, K.; Kan
J. Mol. Biol. 223, 1-7, 1992
A;Title: Gene organization deduced from the complete sequence of liverwort Marchantia po
A;Reference number: S25941; MUID:92114051; PMID:1731062
A;Accession: S25942
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-495 <ODA>
A;Cross-references: UNIPROT:P26848; UNIPARC:UPI0000130771; EMBL:M68929; NID:G786182; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992
R;Nozato, N.; Oda, K.; Yamato, K.; Ohta, E.; Takemura, M.; Akashi, K.; Fukuzawa, H.; Ohy
Mol. Gen. Genet. 237, 343-350, 1993
A;Title: Cotranscriptional expression of mitochondrial genes for subunits of NADH dehydr
A;Reference number: S31171; MUID:93247547; PMID:8483448
A;Accession: S31172
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-495 <NOZ>
A;Cross-references: UNIPARC:UPI0000130771; EMBL:M68929; NID:G786182; PIDN:AAC09398.1; PI
C;Genetics:
A;Gene: nad4
A;Genome: mitochondrion
A;Introns: 183/2
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 4.8%; Score 110; DB 1; Length 495;
Best Local Similarity 18.9%; Pred. No. 0.19;
Matches 78; Conservative 73; Mismatches 152; Indels 110; Gaps 16;

Qy 12 ILALALSMMFTFRFTITLLVHIFISLVILG-----LLFVCGVL 51
Db 130 LIAVFCSLDLLIFVVFVESVLIPMFIIGVMSQRKKAAYQFFLYTLMGSLFMLLAIL 189
Qy 52 WLYYDYTDNLSIELDERENMKCVLGFVAIVSTGITAVLLVLPVLRKRIKLTVELFQIT 111
Db 190 FIFFQTCTDQLLTTE-----FSERQILLMTAFASF 224
Qy 112 NKAISSAPFLLFQPLWTFAILLFPWLWVAVLLSLGTAG----AAQVMEGQVEYKPLSG 167
Db 225 SVKVPVPIVHLPFAHVEAPTAGSVILAGILLKLTGYTFLRFSIPMPEATLYFTP--- 281
Qy 168 IRYMWSYHLIGLIWTSEFILACQOMTIAGAVVTCYFNRSKNPDHPILSSLIFFYHQ 227
```

```
Db 282 --FIYTLSVIAIITYTS--LTTIROIDLKKIIA-----YSSVA-----HM 316
Qy 228 GTVVKGSFLISVVRIPRIIWMYMONALKEQHGALSRYLFRCCYCCFCWCLDKY---LLHL 284
Db 317 NFVTIGMFSLNIOGIEGSILLML-----SHGLVSSALFLCVGALY---DRHKTRIVKY 366
Qy 285 NONAYTTTAINGTDTCTSAKDAFKILSKNSHFTSINCDFDFTIIFLG-----KVLVVCFTV 340
Db 367 YGGLVSTMPITFSTIF-----LFTFLANMSLPCTS-SFIGEFLILVGAFORNSLVATLAA 419
Qy 341 FGGIMAFNYNRAFQVMVAPLLLVAFFA--YLVASHSFLSVFETVLDLALFLCAV 391
Db 420 LGMIL-----GAAYSLMLYNRFVFGNFKPNFILKFSDLNRREVLT---IFLFFIV 465
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Search completed: June 6, 2006, 22:03:49
Job time : 43 secs

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Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

Run on: June 6, 2006, 21:54:45 ; Search time 298 Seconds
(without alignments)
1381.315 Million cell updates/sec

Title: US-10-063-537-32
Perfect score: 2315
Sequence: 1 MSGRDTILGILALSLA.....QQDKSLRNEEGTELOAIVR 445

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 7.2.2*
1: uniprot_sprot*
2: uniprot_trembl*
SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	2314	99.9	605	2 Q7Z6C5 HUMAN	Q7Z6C5 homo sapien
2	2314	99.9	653	1 CTL3 HUMAN	Q8n4m1 homo sapien
3	1857	80.2	652	1 CTL3 MOUSE	Q921v7 mus musculus
4	1854.5	80.1	604	1 CTL3 RAT	Q6ay92 rattus norv
5	1147.5	49.6	651	2 Q632S3_XENLA	Q632s3 xenopus lae
6	1146.5	49.5	651	2 Q61R74_XENLA	Q61r74 xenopus lae
7	1131	48.9	656	1 CTL1 RAT	Q8v1i6 rattus norv
8	1121	48.4	657	1 CTL1 HUMAN	Q8ww15 homo sapien
9	1116	48.2	646	1 CTL1 TORMA	Q919b9 torpedo mar
10	1113	48.1	653	1 CTL1 MOUSE	Q6x893 mus musculus
11	696.5	30.1	493	2 Q7PV56_ANOGA	Q7pv56 anopheles g
12	678	29.3	677	2 Q7QR87_ANOGA	Q7q5r7 anopheles g
13	624.5	27.0	691	2 Q86P33_DROME	Q86p33 drosophila
14	624.5	27.0	691	2 Q9VZE7_DROME	Q9vze7 drosophila
15	611	26.4	707	2 Q6GN42_XENLA	Q6gn42 xenopus lae
16	604.5	26.1	710	2 Q61P59_XENLA	Q61p59 xenopus lae
17	604.5	26.1	863	2 Q4S7S2_TETNG	Q4s7s2 tetraodon n
18	599.5	25.9	704	1 CTL2 MOUSE	Q8by89 mus musculus
19	594.5	25.7	711	1 CTL2 PONY	Q5r519 pongo pygma
20	593.5	25.6	697	2 Q7SYC9_BRARE	Q7sy9c brachydanio
21	593.5	25.6	705	1 CTL2 CAVPO	Q810f1 cavia porce
22	592.5	25.6	723	2 Q7T2B0_BRARE	Q7t2b0 brachydanio
23	590.5	25.5	706	1 CTL2 HUMAN	Q8iwa5 homo sapien
24	583.5	25.2	656	2 Q4T6N2_TETNG	Q4t6n2 tetraodon n
25	571	24.7	628	2 Q54148_DICDI	Q54148 dictyosteli
26	568	24.5	675	2 Q4G0K0_HUMAN	Q4g0k0 homo sapien
27	567	24.5	719	1 CTL5 HUMAN	Q8ncs7 homo sapien
28	555	24.0	717	1 CTL5 MACFA	Q95jw2 macaca fasc
29	544	23.5	710	1 CTL5 MOUSE	Q5rj12 mus musculus
30	539	23.3	710	1 CTL4 HUMAN	Q53gd3 homo sapien
31	538.5	23.3	555	2 Q3TL93_MOUSE	Q3tl93 mus musculus

32	538.5	23.3	707	1 CTL4 MOUSE	Q91val mus musculus
33	538.5	23.3	707	1 Q3ULA4_MOUSE	Q3ula4 mus musculus
34	537.5	23.2	707	1 CTL4 RAT	Q6mg1 rattus norv
35	521.5	22.5	749	2 Q4R1Z5_TETNG	Q4r1z5 tetraodon n
36	513	22.2	796	2 Q9VAP3_DROME	Q9vap3 drosophila
37	509	22.0	773	2 Q618G3_CABER	Q618g3 caenorhabdi
38	505	21.8	730	2 Q8M062_CABER	Q8mq62 caenorhabdi
39	505	21.8	771	2 Q20026_CABER	Q20026 caenorhabdi
40	497.5	21.5	765	2 Q7PRJ0_ANOGA	Q7prj0 anopheles g
41	439	19.0	311	2 Q6NVE7_MOUSE	Q6nve7 mus musculus
42	428	18.5	288	2 Q6UX89_HUMAN	Q6ux89 homo sapien
43	421	18.2	344	2 Q5CZQ9_BRARE	Q5czq9 brachydanio
44	382	16.5	711	2 Q7X668_ORYSA	Q7x668 oryza sativ
45	377	16.3	711	2 Q7XPX3_ORYSA	Q7xpx3 oryza sativ

ALIGNMENTS

RESULT 1
Q7Z6C5_HUMAN PRELIMINARY; PRT; 605 AA.
AC Q7Z6C5;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DE 07-FEB-2006, entry version 12.
DE Hypothetical protein SLC44A3.
GN Name=SLC44A3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M., Soares M.B., Donaldson M.P., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Colon;
RG NIH MCC Project;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
CC EMBL; BC053877; AH53877.1; -; mRNA.
CC Ensembl; ENSG00000143036; Homo sapiens.
CC LinkHub; Q7Z6C5; -
CC InterPro; IPR007603; DUF580.
CC PANTHER; PTHR12385; DUF580; 1.
CC Pfam; PF04515; DUF580; 1.
CC Hypothetical protein.
KW

SQ SEQUENCE 605 AA; 68047 MW; 1182534P9556DADD CRC64;

Query Match 99.9%; Score 2314; DB 2; Length 605;
 Best Local Similarity 99.8%; Pred. No. 2.6e-166;
 Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGRDITLGLCILALALSALSMWTFRTITLLVHIFISLVILGLLFCVGLVWLVYDYTN 60
 DB 161 MSGRDITLGLCILALALSALSMWTFRTITLLVHIFISLVILGLLFCVGLVWLVYDYTN 220

QY 61 DLSIELDTERENMKCVLGFPAIVSTGTAVLLVILFVLRKRIKUTVLFQITNKAISSAPP 120
 DB 221 DLSIELDTERENMKCVLGFPAIVSTGTAVLLVILFVLRKRIKUTVLFQITNKAISSAPP 280

QY 121 LIFQPLWTTAILIFFVWLVAVLLSGLTAGAAQWEGGVVEKPLSGIRYMSYHLIGLI 180
 DB 281 LIFQPLWTTAILIFFVWLVAVLLSGLTAGAAQWEGGVVEKPLSGIRYMSYHLIGLI 340

QY 181 WTSEFLACQOMTIAGAVVTCYFNRSKNDDPPDHPILSSLSILFFYHOGTVWKSFLISVV 240
 DB 341 WTSEFLACQOMTIAGAVVTCYFNRSKNDDPPDHPILSSLSILFFYHOGTVWKSFLISVV 400

QY 241 RIPRIIVMYQNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVYTTAINGTDFC 300
 DB 401 RIPRIIVMYQNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVYTTAINGTDFC 460

QY 301 TSAKDAPKILSKNSHFTSINCEGDEIIFLGKVLVVCFTVFGGLMAFNYNRAFOQWAVPL 360
 DB 461 TSAKDAPKILSKNSHFTSINCEGDEIIFLGKVLVVCFTVFGGLMAFNYNRAFOQWAVPL 520

QY 361 LLVAFAYLVAHSFLSVFETVLDALFLCPAVDLETNDGSEKPYFMDQBFLSFVKRSNKL 420
 DB 521 LLVAFAYLVAHSFLSVFETVLDALFLCPAVDLETNDGSEKPYFMDQBFLSFVKRSNKL 580

QY 421 NNARAQDKHSLRNEEGTELOAIVR 445
 DB 581 NNARAQDKHSLRNEEGTELOAIVR 605

RESULT 2

CTL3_HUMAN STANDARD; PRT; 653 AA.

AC Q8N4M1; Q9BWY7;
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 30-AUG-2005, sequence version 3.
 DT 07-MAR-2006, entry version 15.
 DE Choline transporter-like protein 3 (Solute carrier family 44 member 3).
 GN Names=SLC4A3; Synonyms=CTL3; ORFNames=UNQ558/PRO1115;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RG Human chromosome 1 international sequencing consortium;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC TISSUE=Brain, and Colon;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins L.S., Wagner K.H., Shenmen C.M., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Smailus D.E., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Marra M.A., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 147-653, AND VARIANT VAL-438.
 RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
 RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D.T., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J.S., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao M.R., Mark M.R., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R.L., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.G., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A.D., Wood W.I., Godowski P.J., Gray A.M.;
 RA "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
 RL Genome Res. 13:2265-2270 (2003).
 RN [4]
 RP IDENTIFICATION, AND NOMENCLATURE.
 RX MEDLINE=20144127; PubMed=10677542; DOI=10.1073/pnas.030339697;
 RA O'Regan S., Traifet E., Ruat M., Cha N., Compaore D., Meunier F.-M.;
 RT "An electric lobe suppressor for a yeast choline transporter mutation belongs to a new family of transporter-like proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1835-1840 (2000).
 CC -!- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 CC EMBL; AC093429; -; NOT ANNOTATED_CDS; Genomic_DNA.
 DR EMBL; AL359554; CAC36091.1; -; Genomic DNA.
 DR EMBL; BC033858; AAH33858.2; ALT INIT; mRNA.
 DR EMBL; AY358659; AAQ89022.1; ALT INIT; mRNA.
 DR Ensembl; ENSG00000143036; Homo sapiens.
 DR HGNC; HGNC:28689; SLC4A3.
 DR InterPro; IPR007603; DUF580.
 DR Pfam; PF04515; DUF580; 1.
 DR Membrane; Polymorphism; Transmembrane.
 KW CHAIN 1 653 Choline transporter-like protein 3.
 FT FTId=PRO_0000191720.
 FT TRANSMEM 34 54 Potential.
 FT TRANSMEM 213 233 Potential.
 FT TRANSMEM 243 263 Potential.
 FT TRANSMEM 284 304 Potential.
 FT TRANSMEM 334 354 Potential.
 FT TRANSMEM 384 404 Potential.
 FT TRANSMEM 428 448 Potential.
 FT TRANSMEM 534 554 Potential.
 FT TRANSMEM 563 583 Potential.
 FT VARIANT 438 438 I -> V (in dbSNP:rs59098).
 FT /FTId=VAR_023405.
 FT CONFLICT 465 465 Missing (in Ref. 1; CAC36091).
 FT SEQUENCE 653 AA; 73797 MW; 54807C920086427B CRC64;

Query Match 99.9%; Score 2314; DB 1; Length 653;
 Best Local Similarity 99.8%; Pred. No. 2.8e-166;
 Matches 444; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGRDITLGLCILALALSALSMWTFRTITLLVHIFISLVILGLLFCVGLVWLVYDYTN 60
 DB 209 MSGRDITLGLCILALALSALSMWTFRTITLLVHIFISLVILGLLFCVGLVWLVYDYTN 268

QY 61 DLSIELTERENKCVLGFPAIVSTGITAVLLVLFVLRKRIKLTVELFOITNKAISSAPP 120
 Db 269 DLSIELTERENKCVLGFPAIVSTGITAVLLVLFVLRKRIKLTVELFOITNKAISSAPP 328
 QY 121 LLFQPLMTFAILIFFFWLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLI 180
 Db 329 LLFQPLMTFAILIFFFWLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLI 388
 QY 181 WTSEFIIACQOMTITAGAVVTCYFNRSKNDPPDHPILSSILFFYHOGTVVKGSLISV 240
 Db 389 WTSEFIIACQOMTITAGAVVTCYFNRSKNDPPDHPILSSILFFYHOGTVVKGSLISV 448
 QY 241 RIPRIIVMYQNALKEOQHGSALSYLRCCVCCFWCLDKYLLHLNQAYTTTANGTDFC 300
 Db 449 RIPRIIVMYQNALKEOQHGSALSYLRCCVCCFWCLDKYLLHLNQAYTTTANGTDFC 508
 QY 301 TSAKDAFKILSKNSHSTINCFDGFIIIFLGKLVVCFVFGGLMAFNRAFOVAVPL 360
 Db 509 TSAKDAFKILSKNSHSTINCFDGFIIIFLGKLVVCFVFGGLMAFNRAFOVAVPL 568
 QY 361 LLVAFPAVLVAHSLVSVFETVLDALFLCFAVDLETNDGSEKPYFMDQEFSLFVKRSNKL 420
 Db 569 LLVAFPAVLVAHSLVSVFETVLDALFLCFAVDLETNDGSEKPYFMDQEFSLFVKRSNKL 628
 QY 421 NNARAQODKHSRNEEGTELOAIVR 445
 Db 629 NNARAQODKHSRNEEGTELOAIVR 653

RESULT 3
 CTL3_MOUSE
 ID CTL3_MOUSE STANDARD; PRT; 652 AA.
 AC Q921V7;
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 30-AUG-2005, sequence version 2.
 DT 07-MAR-2006, entry version 27.
 DE Choline transporter-like protein 3 (Solute carrier family 44 member
 DE 3).
 GN Name=Slc44a3; Synonyms=Ctl3;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;
 RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Viallon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -|- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
 CC similarity).
 CC -|- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
 CC

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 CC EMBL; BC010552; AAH10552.1; ALT INIT; mRNA.
 CC EMBL; BC025548; AAR25548.1; ALT INIT; mRNA.
 DR Ensembl; ENSMUSG00000039865; Mus musculus.
 DR MGI; MGI:2384860; Slc44a3.
 DR InterPro; IPR007603; DUF580.
 DR Pfam; PF04515; DUF580; 1.
 KW Membrane; Transmembrane.
 FT CHAIN 1 652
 FT TRANSMEM 33 53
 FT TRANSMEM 212 232
 FT TRANSMEM 238 258
 FT TRANSMEM 284 304
 FT TRANSMEM 333 353
 FT TRANSMEM 377 397
 FT TRANSMEM 533 553
 FT TRANSMEM 562 582
 SQ SEQUENCE 652 AA; 73028 MW; A0DA359C7509C8B3 CRC64;
 Query Match 80.2%; Score 1857; DB 1; Length 652;
 Best Local Similarity 78.4%; Pred. No. 9.4e-132;
 Matches 349; Conservative 39; Mismatches 57; Indels 0; Gaps 0;
 QY 1 MSGRDTILGLCILALSLAMMTFRITTLVHIFISLVILGLLFCVGVLMWLYDYDTN 60
 Db 208 MAGRDTILGLCVFTFALSLAMLFAPRISTLLHIIISLVILGLLFCVGVLMWLYDYDTN 267
 QY 61 DLSIELTERENKCVLGFPAIVSTGITAVLLVLFVLRKRIKLTVELFOITNKAISSAPP 120
 Db 268 DLSIELTERENKCVLGFPAIVSTGITAVLLVLFVLRKRIKLTVELFOITNKAISSAPP 327
 QY 121 LLFQPLMTFAILIFFFWLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLI 180
 Db 328 LLFQPLMTFAILIFFFWLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLI 387
 QY 181 WTSEFIIACQOMTITAGAVVTCYFNRSKNDPPDHPILSSILFFYHOGTVVKGSLISV 240
 Db 388 WTSEFIIACQOMTITAGAVVTCYFNRSKNDPPDHPILSSILFFYHOGTVVKGSLISV 447
 QY 241 RIPRIIVMYQNALKEOQHGSALSYLRCCVCCFWCLDKYLLHLNQAYTTTANGTDFC 300
 Db 448 RIPRIIVMYQNALKEOQHGSALSYLRCCVCCFWCLDKYLLHLNQAYTTTANGTDFC 507
 QY 301 TSAKDAFKILSKNSHSTINCFDGFIIIFLGKLVVCFVFGGLMAFNRAFOVAVPL 360
 Db 508 TSAKDAFKILSKNSHSTINCFDGFIIIFLGKLVVCFVFGGLMAFNRAFOVAVPL 567
 QY 361 LLVAFPAVLVAHSLVSVFETVLDALFLCFAVDLETNDGSEKPYFMDQEFSLFVKRSNKL 420
 Db 568 LLVAFPAVLVAHSLVSVFETVLDALFLCFAVDLETNDGSEKPYFMDQEFSLFVKRSNKL 627
 QY 421 NNARAQODKHSRNEEGTELOAIVR 445
 Db 628 NNARAQODKHSRNEEGTELOAIVR 652
 RESULT 4
 CTL3_RAT
 ID CTL3_RAT STANDARD; PRT; 604 AA.
 AC Q6AY92;
 DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
 DT 13-SEP-2004, sequence version 1.
 DT 07-FEB-2006, entry version 16.
 DE Choline transporter-like protein 3 (Solute carrier family 44 member
 DE 3).
 GN Name=Slc44a3; Synonyms=Ctl3;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridea; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;

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RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Kidney;
RG NIH - Mammalian Gene Collection (MGC) project;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
[2]
RN TISSUE SPECIFICITY.
RC STRAIN=Wistar; TISSUE=Brain;
RX PubMed=15715662; DOI=10.1111/j.1471-4159.2004.02962.x;
RA Traillfort E., Ruat M., O'Regan S., Meunier F.-M.;
RT "Molecular characterization of the family of choline transporter-like
RL J. Neurochem. 92:1116-1125(2005).
CC -i- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By
CC similarity).
CC -i- TISSUE SPECIFICITY: Expressed in colon, kidney and ileum.
CC -i- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
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[1]
DR EMBL; BC079142; AAH79142.1; -; mRNA.
DR RGD; 1305808; Ctl3.
DR InterPro; IPR007603; DUF580.
DR PANTHER; PTHR12385; DUF580; 1.
DR Pfam; PF04515; DUF580; 1.
DR KEGG; Membrane; Transmembrane.
FT CHAIN 1 604 Choline transporter-like protein 3.
FT FTID=PRO_0000191722.
FT TRANSMEM 165 185 Potential.
FT TRANSMEM 195 215 Potential.
FT TRANSMEM 237 257 Potential.
FT TRANSMEM 286 306 Potential.
FT TRANSMEM 330 350 Potential.
FT TRANSMEM 485 505 Potential.
FT TRANSMEM 514 534 Potential.
FT SEQUENCE 604 AA; 67679 MW; BA47C3A411CE3E1B CRC64;
SQ
Query Match 80.1%; Score 1854.5; DB 1; Length 604;
Best Local Similarity 78.4%; Pred. No. 1.3e-131;
Matches 349; Conservative 37; Mismatches 58; Indels 1; Gaps 1;
QY 1 MSGRDTILGICILALALSMMFTFRITTLVHIFISLVILGLFVCGVWMLVYDYTN 60
DB 161 MAGRDITLGLCAVFAFALSAMLTFRISTLVAHIIISLVILGLFVCGVFWMLVYDYTN 220
QY 61 DLSIELDTERENKCVLGFPAIVSTGTVAVLLVIFVLRKRIKLTVELFQITNKAISAPF 120
DB 221 DLSIELDTENKMKCLAFAVITVTVVLLALIFTLRKRKVLTVELLRVTNKAISRCPP 280
QY 121 LLFQPLWTFAILIFFWVWVAVLLSLGTAGAAQVMGGQVEYKPLSGIRYMWVYHLIGLI 190
DB 281 LLFQPLWTFAILVFWVWVAVLLSLGTAGTAQVMGGQVEYKPLSGIRYLMWYHLIGLI 340
QY 181 WTSEFILAQOMTIAGAVVTTCYFNRSKNDDPDPHPILSSLSILFFYHOGTVVKGSLISVV 240
DB 341 WTSEFILTQRMVTVAGMWVTCYFNQNDDPPAPILSSLSLTLCYHOGTVAKGSLLTVT 400
QY 241 RPIRIIVMYQNALKEQHQGALGRYLFRCYCCFCWCLDKYLLHLNQNAVYTTAINGTDFC 300
DB 401 RPIRVIFMYIYSTVKE-RHSAPRGPFRCSYCYGLWCLTNPYPHLNQDAVAAAAINGTDFC 459
QY 301 TSAKDAFKILSKNSHFTSINCEGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVAVPL 360
DB 460 TSAKDAHTIISKNSHLSITVNCFGNFIFLGKVLVVCFTVFGGLMAFNYNRAQVAVPL 519
QY 361 LLVAFAYLVAHFSLSVFETVLDALFLCFVAVDTETNDGSEKPYFMDQEPFLSVKRSNKL 420
DB 520 LLVAFAYLAAHFSLSVFETVLDALFLCFVAVDTETNDGSEKPYFMDQEPFLSVKRTDHF 579
QY 421 NNARAQDKHSLNREGTELQAVIR 445
DB 580 NNARSQGHKNSLPNEEGTELRPIVR 604
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RESULT 5
Q632S3_XENLA PRELIMINARY; PRT; 651 AA.
AC Q632S3;
DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
DT 25-OCT-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE MGC82240 protein.
GN Name=MGC82240;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Scherich A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Klein S., Gerhard D.S.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
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[1]
DR EMBL; BC082837; AAH82837.1; -; mRNA.
DR InterPro; IPR007603; DUF580.
DR PANTHER; PTHR12385; DUF580; 1.
DR Pfam; PF04515; DUF580; 1.
SQ SEQUENCE 651 AA; 72937 MW; A26613B3055420AF CRC64;
Query Match 49.6%; Score 1147.5; DB 2; Length 651;
Best Local Similarity 49.6%; Pred. No. 3.8e-78;
Matches 221; Conservative 85; Mismatches 127; Indels 13; Gaps 4;
QY 1 MSGRDTILGICILALALSMMFTFRITTLVHIFISLVILGLFVCGVWMLVYDYTN 60
DB 205 MTSKEILMGLCLLSVLMSLVITIRYISRLVITITLVLSGLGCTGVWMLVADNKK 264
QY 61 DLS-----IELDTERENKCVLGFPAIVSTGTVAVLLVIFVLRKRIKLTVELFQITNKA 115
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Db 265 SLNENLPDQOVSKDNLQALLVVAIAATVFTVILLMLLMRKREVALTIALFNVAGKVF 324
Qy 116 SSAPFLFPQPLWTFATILFFVVLVAVLLSFTAGAAQVMEGGQVEYKPLSGIRYMSYH 175
Db 325 IHLPLLVFPQPTWTFALLFWVYVWVLLFGLTAGDPTNEQGFVERINGPLQYMWYH 384
Qy 176 LIGLWTSFIFLACQMTIAGAVTCTPNRSKNDPPDHPILSSLSILFFHQGVVKGSP 235
Db 385 LVGLWISFIFLACQMTIAGAVTCTPNRSKNDPPDHPILSSLSILFFHQGVVKGSP 235
Qy 236 LISVVRIPRIIVMYMGNALKEOQHGSRLVFCYCCFWCLDKVYLHLNQNAYTTAIN 295
Db 445 IITLVKIPRILMYIHSQKGEN-ACARCMLKSCICCLWCKLEKCLAYLNQNAYTTAIN 503
Qy 296 GTDFCTSAKDAFKILSKNSHFTSINCFCGDFIIFLGLKVLVVCFTVFGGLMAFNRAFOV 355
Db 504 STNFTCSAKDALVILVENALRVAAINTVGDPMFLGKILIVSCITGLAGIMLLNQYDVT 563
Qy 356 WAVPLLVAFAYLVVAHSFVSFTVLDALFLCFPAVDLETDNGSSEKPYFMDQEFVSK 415
Db 564 WVLPLIIVCLFAFLVAHCFLSIYEMVVDVLFCLFAIDTKYNDGSPGKEFYMDKVLMEFVE 623
Qy 416 RSNKLNARAQODKHSRLNEBGETLO 441
Db 624 DSR-----RALKEPGS--TAEGRELK 642

RESULT 6
Q6IR74_XENLA
ID Q6IR74_XENLA PRELIMINARY; PRT; 651 AA.
AC Q6IR74;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE MGC82240 protein.
GN Name=MGC82240;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22368257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Henchen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uadin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
```

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RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
[3]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Kidney;
RA Klein S., Strausberg R.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC071026; AAH71026.1; -; mRNA.
DR InterPro; IPR007603; DUF580.
DR PANTHER; PTHR12385; DUF580; 1.
DR Pfam; PF04515; DUF580; 1.
SQ SEQUENCE 651 AA; 72908 MW; 619A2CB2C848FOAF CRC64;

Query Match 49.5%; Score 1146.5; DB 2; Length 651;
Best Local Similarity 49.6%; Pred. No. 4.5e-77;
Matches 221; Conservative 85; Mismatches 127; Indels 13; Gaps 4;

Qy 1 MSGRDTILGLCILALALSAMMTFTTITLLVHIFISLVILGLLFCVGLWMLLYDYN 60
Db 205 MTSKEIIMGLCLSLVLSMLMIIRYISRVLWITILVVLGSLGTGVLWMLYADNKK 264
Qy 61 DLS-----IELDTERENMKCVLGAIVSTGITAVLLVILFVLRKRIRKLTVELFOITNKA 115
Db 265 SLNENLPDQOVSKDNLQALLVVAIAATVFTVILLMLLMRKREVALTIALFNVAGKVF 324
Qy 116 SSAPFLFPQPLWTFATILFFVVLVAVLLSFTAGAAQVMEGGQVEYKPLSGIRYMSYH 175
Db 325 IHLPLLVFPQPTWTFALLFWVYVWVLLFGLTAGDPTNEQGFVERINGPLQYMWYH 384
Qy 176 LIGLWTSFIFLACQMTIAGAVTCTPNRSKNDPPDHPILSSLSILFFHQGVVKGSP 235
Db 385 LVGLWISFIFLACQMTIAGAVTCTPNRSKNDPPDHPILSSLSILFFHQGVVKGSP 235
Qy 236 LISVVRIPRIIVMYMGNALKEOQHGSRLVFCYCCFWCLDKVYLHLNQNAYTTAIN 295
Db 445 IITLVKIPRILMYIHSQKGEN-ACARCMLKSCICCLWCKLEKCLAYLNQNAYTTAIN 503
Qy 296 GTDFCTSAKDAFKILSKNSHFTSINCFCGDFIIFLGLKVLVVCFTVFGGLMAFNRAFOV 355
Db 504 STNFTCSAKDALVILVENALRVAAINTVGDPMFLGKILIVSCITGLAGIMLLNQYDVT 563
Qy 356 WAVPLLVAFAYLVVAHSFVSFTVLDALFLCFPAVDLETDNGSSEKPYFMDQEFVSK 415
Db 564 WVLPLIIVCLFAFLVAHCFLSIYEMVVDVLFCLFAIDTKYNDGSPGKEFYMDKVLMEFVE 623
Qy 416 RSNKLNARAQODKHSRLNEBGETLO 441
Db 624 DSR-----RALKEPGS--TAEGRELK 642

RESULT 7
CTLL1_RAT
ID CTLL1_RAT STANDARD; PRT; 656 AA.
AC Q8V1I6; Q9JUZ7;
DT 30-AUG-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-MAR-2002, sequence version 1.
DT 07-MAR-2006, entry version 21.
DE Choline transporter-like protein 1 (Solute carrier family 44 member 1)
DE (CD92 antigen) (CDw92).
GN Names=Slc44a1; Synonyms=Cdw92, Ctll1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2), AND TISSUE SPECIFICITY.
RC TISSUE=Brain;
RX MEDLINE=20144127; PubMed=10677542; DOI=10.1073/pnas.030339697;
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OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND ALTERNATIVE SPLICING (ISOFORM 2).
 RC TISSUE=Ewing sarcoma;
 RX MEDLINE=2014127; PubMed=10677542; DOI=10.1073/pnas.03039697;
 O'Regan S., Traiffort E., Ruat M., Cha N., Compaore D., Meunier F.-M.;
 RT "An electric lobe suppressor for a yeast choline transporter mutation belongs to a new family of transporter-like proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:1835-1840(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 3), AND TISSUE SPECIFICITY.
 RX MEDLINE=2155187; PubMed=11698453;
 RA Wille S., Sezeres A., Majdic O., Prager E., Staffler G., Stoeckl J.,
 RA Klunghaler D., Prieschl E.E., Baumrucker T., Burtscher H.,
 RA Zlabinger G.J., Knapp W., Stockinger H.;
 RT "Characterization of Cdw92 as a member of the choline transporter-like protein family regulated specifically on dendritic cells.";
 RL J. Immunol. 167:15795-15804(2001).
 RN [3]
 RP NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 1).
 RC TISSUE=Ewing sarcoma;
 RX PubMed=15715662; DOI=10.1111/j.1471-4159.2004.02962.x;
 RA Traiffort E., Ruat M., O'Regan S., Meunier F.-M.;
 RT "Molecular characterization of the family of choline transporter-like proteins and their splice variants.";
 RL J. Neurochem. 92:1116-1125(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RX PubMed=15164053; DOI=10.1038/nature02465;
 RA Humphray S.J., Oliver K., Hunt A.R., Plumb R.W., Loveland J.E.,
 RA Howe K.L., Andrews T.D., Searle S., Hunt S.E., Scott C.B., Jones M.C.,
 RA Ainscough R., Almeida J.P., Ambrose K.D., Ashwell R.I.S.,
 RA Babbage A.K., Babbage S., Bauguley C.L., Bailey J., Banerjee R.,
 RA Barker D.J., Barlow K.F., Bates K., Beasley H., Beasley O., Bird C.P.,
 RA Bray-Allen S., Brown A.J., Brown J.K., Burford D., Burfill W.,
 RA Burton J., Carder C., Carter N.P., Chapman J.C., Chen Y., Clarke G.,
 RA Clark S.Y., Clee C.M., Clegg S., Collier R.E., Corby N., Crosier M.,
 RA Cummings A.T., Davies J., Dhani P., Dunn M., Dutta I., Dyer L.W.,
 RA Edmunds M.E., Faulkner L., Fleming C.J., Frankish A.,
 RA Frankland J.A., French L., Fricker D.G., Garner P., Garnett J.,
 RA Ghori J., Gilbert J.G.R., Gilson C., Grafham D.V., Gribble S.,
 RA Griffiths C., Griffiths-Jones S., Grocock R., Guy J., Hall R.E.,
 RA Hammond S., Harley J.L., Harrison E.S.I., Hart E.A., Heath P.D.,
 RA Henderson C.D., Hopkins B.L., Howard P.J., Howden P.J., Huckle E.,
 RA Johnson C., Johnson D., Joy A.A., Kay M., Keenan S., Kershaw J.K.,
 RA Kimberley A.M., King A., Knights A., Laird G.K., Langford C.,
 RA Lawlor S., Leongamornlert D.A., Levensha M., Lloyd C., Lloyd D.M.,
 RA Lovell J., Martin S., Mashreghi-Mohammadi M., Matthews L., McLaren S.,
 RA McLay K.E., McMurray A., Milne S., Nickerson T., Nisbett J.,
 RA Nordsiek G., Pearce A.V., Peck A.I., Porter K.M., Pandian R.,
 RA Peltan S., Phillimore B., Povey S., Ramsey Y., Rand V., Scharfe M.,
 RA Shera H.K., Showkeen R., Sims S.K., Skuce C.D., Smith M.,
 RA Steward C.A., Swardbeck D., Sycamore N., Tester J., Thorpe A.,
 RA Tracey A., Tromans A., Thomas D.W., Wall M., Wallis J.M., West A.P.,
 RA Whitehead S.L., Willey D.L., Williams S.A., Wilming L., Wray P.W.,
 RA Young L., Ashurst J.L., Coulson A., Blocker H., Durbin R.,
 RA Sulston J.E., Hubbard T., Jackson M.J., Bentley D.R., Beck S.,
 RA Rogers J., Dunham I.;
 RT "DNA sequence and analysis of human chromosome 9.";
 RL Nature 429:369-374(2004).
 RN [5]
 RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
 RC TISSUE=Eye, and Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshlyuk S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Probable choline transporter. May be involved in membrane synthesis and myelin production (By similarity).
 CC -1- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=A;
 CC IsoId=Q8WWI5-1; Sequence=Displayed;
 CC Name=2; Synonyms=B;
 CC IsoId=Q8WWI5-2; Sequence=VSP_015424, VSP_015425;
 CC Name=3; Synonyms=C;
 CC IsoId=Q8WWI5-3; Sequence=VSP_015426, VSP_015427;
 CC -1- TISSUE SPECIFICITY: Expressed in various cells of the hematopoietic system.
 CC -1- SIMILARITY: Belongs to the CTL (choline transporter-like) family.
 CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
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 DR EMBL; AJ275620; CAB75541.2; -; Genomic DNA.
 DR EMBL; AJ272365; CAC82175.1; -; mRNA.
 DR EMBL; AJ420812; CAD12764.1; -; Genomic DNA.
 DR EMBL; AL161627; CAI13069.1; -; Genomic DNA.
 DR EMBL; AL450265; CAI13069.1; JOINED; Genomic DNA.
 DR EMBL; AL590368; CAI13069.1; JOINED; Genomic DNA.
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 DR EMBL; AL161627; CAH73434.1; -; Genomic DNA.
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 DR EMBL; AL450265; CAH73435.1; JOINED; Genomic DNA.
 DR EMBL; AL590368; CAH73435.1; JOINED; Genomic DNA.
 DR EMBL; AL161627; CAH73436.1; -; Genomic DNA.
 DR EMBL; AL450265; CAH73436.1; JOINED; Genomic DNA.
 DR EMBL; BC018213; AAH18213.1; -; mRNA.
 DR EMBL; BC049203; AAH49203.1; -; mRNA.
 DR Ensemble; ENSG00000070214; Homo sapiens.
 DR HGNC; HGNC:18798; SLC44A1.
 DR MIM; 606105; gene.
 DR InterPro; IPR007603; DUF580.
 DR PANTHER; PTHR12385; DUF580; 1.
 DR Pfam; PF04515; DUF580; 1.
 KW Alternative splicing; Antigen; Membrane; Transmembrane; Transport.
 CHAIN 1 657 /FTId=PRO_0000191712.
 FT

Query Match		48.2%; Score 1116; DB 1; Length 646;
Best Local Similarity		48.3%; Pred. No. 9e-76;
Matches 204; Conservative		89; Mismatches 125; Indels 4; Gaps 2;
QY	1	MSGRDITGLHCIALALSLAMMFTFRITTLVHIFISLVILGLFVCGVLMWLYDYDTN 60
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QY	61	DLSEL---DTERENMKVGLGFAIVSGITAVLAVLIFVLKRIKLVFELFQITNKAISS 117
DB	264	TLKLDPQSGDAADNVTALEVCALIAITVITVILLMLINKRVALTIALFHVAGKFIH 323
QY	118	APELLFPLATFALLIFPWLWVAVLSLGTAGNAQWMEGQVEYKPLSGIRYMWVHLI 177
DB	324	IPFLIFOSLTFALAFWIIYIAVALLATAGYPQKQDQYVEFKVSGPLQYTWIYHLV 383
QY	178	GLIWTSEFILACQOMTAGAVWTCYFNRSKNRDPDHPILSLSLIFPYHOGTVKGSFLI 237
DB	384	GLIWISEFILACQOMTAGAVWTVYFTRDKNLPATFILASMKELIKYHLGTWAKGSFII 443
QY	238	SVVRIPRIIVMYQNALKEQOHGALSRYLPCRCYCCFCWCLDKVLLHLNQNAYTTTAINGT 297
DB	444	TLIKIPQMLVYIHSQKGRN-ACAKCMLKACWCLWCKLEKCLLYLRNAYIATSINGT 502
QY	298	DFCTSAKDAFKILSKNSHTSINCFDGFIFIGKVLVVCFTVFGGLMAFNARAFQVWA 357
DB	503	SFCTSAKDAIVLVENARVAANTVGDVFLFKLLIVLTVGFGVIGILLNYORDYTVWV 562
QY	358	VPLLVAFFAVLVAHSFLSVFETVLDALFLCFADVLETDNGSSEKPKVFMDOEFLSVKRS 417
DB	563	LPIIICLFAFFVSHCFLSIYMWVVDVFLCFADVCKHNDGSPGREYIMDKSLMEFMDSES 622
QY	418	NK 419
DB	623	RK 624
RESULT 10		
CTLI MOUSE		
ID	CTLI_MOUSE	STANDARD; PRT; 653 AA.
AC	Q6X893; Q6X894; Q8R0V4; Q91Z29;	
DT	30-AUG-2005, integrated into UniProtKB/Swiss-Prot.	
DT	07-MAR-2006, entry version 15.	
DE	Choline transporter-like protein 1 (Solute carrier family 44 member 1) (CD92 antigen) (CDw92).	
GN	Name=Slc44a1; Synonyms=Cdw92, Ctl1;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;	
OC	Muroidea; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS 1 AND 2), TISSUE SPECIFICITY,	
RP	SUBCELLULAR LOCATION, AND FUNCTION.	
RC	TISSUE=Brain; Fibrinogen;	
RA	Yuan Z., Wagner L., Polomienko A., Bakovic M.;	
RT	"Identification and expression of a mouse muscle-specific CTL1 gene.";	
RL	Gene 341:305-312(2004).	
RN	[2]	
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] OF 390-653 (ISOFORM 1).	
RP	STRAIN=FVB/N; TISSUE=Liver, and Mammary gland;	
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Whiting J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	
RA	Schurber A., Schein J.E., Jones S.J.M., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length human	
RT	and mouse cDNA sequences.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
CC	- FUNCTION: Probable choline transporter. May be involved in	
CC	membrane synthesis and myelin production.	
CC	- SUBCELLULAR LOCATION: Membrane; multi-pass membrane protein.	
CC	- ALTERNATIVE PRODUCTS:	
CC	Event=Alternative splicing; Named isoforms=2;	
CC	Name=1; Synonyms=A;	
CC	ISOIDS=Q6X893-1; Sequence=Displayed;	
CC	Name=2; Synonyms=B;	
CC	ISOIDS=Q6X893-2; Sequence=VSP_015428;	
CC	- TISSUE SPECIFICITY: Specifically abundant in skeletal muscle (at	
CC	protein level).	
CC	- SIMILARITY: Belongs to the CTL (choline transporter-like) family.	
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms	
CC	Distributed under the Creative Commons Attribution-NoDerivs License	
CC	-----	
EMBL	AY249865; AAP81042.1; -; mRNA.	
DR	ENBL; AY249866; AAP81043.1; -; mRNA.	
DR	ENBL; BC010258; AAH10258.1; -; mRNA.	
DR	ENBL; BC025941; AAH25941.1; ALT_INIT; mRNA.	
DR	Ensembl; ENSMUSG0000028412; MMTUSCUT.	
DR	MGI; MGI:2140592; SLC44a1.	
DR	GO; GO:0016021; C:integral to membrane; IDA.	
DR	GO; GO:0015220; F:choline transporter activity; IDA.	
DR	GO; GO:0015871; P:choline transport; IDA.	
DR	InterPro; IPR007603; DUF580.	
DR	Pfam; PF04515; DUF580; 1.	
KW	Alternative splicing; Membrane; Transmembrane; Transport.	
CHAIN	1 653	
FT	TOPO_DOM 1 29	
FT	TRANSMEM 30 50	
FT	TOPO_DOM 51 211	
FT	TRANSMEM 212 232	
FT	TOPO_DOM 233 237	
FT	TRANSMEM 238 258	
FT	TOPO_DOM 259 287	
FT	TRANSMEM 288 308	
FT	TOPO_DOM 309 314	
FT	TRANSMEM 315 335	
FT	TOPO_DOM 336 337	
FT	TRANSMEM 338 358	
FT	TOPO_DOM 359 379	
FT	TRANSMEM 380 400	
FT	TOPO_DOM 401 441	
FT	TRANSMEM 442 462	
FT	TOPO_DOM 463 536	
FT	TRANSMEM 537 557	
FT	TOPO_DOM 558 565	
FT	TRANSMEM 566 586	
FT	TOPO_DOM 587 653	
FT	COMPTIAS 473 491	
FT	VARSPLIC 650 653	
FT	isoform 2) /FTIDA=VSP_015428.	
FT	L -> P (in Ref. 2; AAH25941).	
FT	F -> L (in Ref. 2; AAH25941).	
FT	L -> F (in Ref. 2; AAH25941).	
SQ	SEQUENCE 653 AA; 73083 MW; 3857DA8BE428EFP5 CRC64;	
Query Match		48.1%; Score 1113; DB 1; Length 653;

[illegible]

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RESULT 11
Q7PY56 ANOGA
ID Q7PY56 ANOGA PRELIMINARY; PRT; 493 AA.
AC Q7PY56;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 06-DEC-2005, sequence version 2.
DT 07-FEB-2006, entry version 10.
DE ENSANGP00000112864 (Fragment).
GN ORFNames=ENSANGG000000110375;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL "Anopheles gambiae re-annotation.";
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
-----
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-----
CC
CC ENBL; AAB01008987; EAA01239.2; -; Genomic_DNA.
DR
DR PANTHER; PTHR12385; DUF580; 1.
DR NON TER 1
DR NON TER 493 493
SO SEQUENCE 493 AA; 55842 MW; 99A8AF97E70134BB CRC64;

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Query Match	30.13;	Score	696.5;	DB	2;	Length	493;
Best Local Similarity	37.23;	Pred. No.	3.4e-44;				
Matches	159;	Conservative	84;	Mismatches	169;	Indels	15;
Gaps	8;						
Qy	10	LCIALALSLAMMPTFRFITTLVHIFISILVILGLLFCV--GVLW-WLYDYDTND--LSI	64				
Db	63	LAVTAFASLLTLVLLRVIPGLIIVW---LVLLAVVLACTAGTITWLMRMQYEAHLP	118				
Qy	65	ELDTERENMKCVLGFPAIVSTGITAVLVLVFLVKRKIKLTVLQITNKAISSAPFL	124				
Db	119	AADSSRMNNWLYAYAAATVATLLVVLVILVMKRIKLVVQLPKERAKAIASMPFL	178				
Qy	125	PLMTFAILLFPFVLWVAVLLSLGTAGAAQYMEGQVEYKPLSGIRYVWMSYHLIGLI	184				
Db	179	PILTFAIAAIVLVVYFTVWIESAGMLVNESNNAKYVKDSTMLFTRWYNLFAFLW	238				
Qy	185	FILACQMTIAGAVVTCYFNRSKNDPDHPILSLSLFFVHQGTUVKGSFLISVVRIP	244				
Db	239	FVIGCQHMVIAGAVAGFFTRNKS--LSNPIGRSYCNLLRYHLGTVALGSGFVIAL	297				
Qy	245	IIVMYMONALKEQOHGALSRFLPCCYCCFWCLDKYLLHLNQNAYTTAINGDTFC	304				
Db	298	AMLKLLMHSVRNPQVRVTS--FLPCCQCCQCPEFLQYLTRNAYILTAHMGDP	356				
Qy	305	DAFKILSKNSHFTSINCFGDIFILGKVLVCTVTFGGLMAFNYNRAQFQWAVPL	364				
Db	357	NAFRLTLNNALRVPAINSVGDVFLVLAQVFWVATGLIGVELIKQKVGCLHHPPY	416				
Qy	365	FFAVLVHVSFLSVPETVLDALFLCFAVDLETNDGSSEKPFMDQEFLSFVKRS	424				
Db	417	IFALVLAHCWFVTEMVTDIFLCFCDECSNDGIS-RPYVMSGLMEFVQNSK--	472				
Qy	425	AQQDKHS	431				
Db	473	SIADKSS	479				

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RESULT 12
Q7QSR7 ANOGA PRELIMINARY; PRT; 677 AA.
ID Q7QSR7 ANOGA
AC Q7QSR7;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 07-DEC-2004, sequence version 2.
DT 07-FEB-2006, entry version 10.
DE ENSANGP00000020538 (Fragment).
GN ORFNames=ENSANGG00000018049;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Anophelinae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG "The Anopheles gambiae Sequence Committee;
RT "Anopheles gambiae re-annotation.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PEST;
RG The Anopheles gambiae Sequence Committee;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
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CC -----
CC EMBL; AAAB01008960; EAA10766.2; -; Genomic_DNA.
CC InterPro; IPR007603; DUF580.
CC PANTHER; PTHR12385; DUF580; 1.

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DR	Pfam; PF04515; DUF580; 1.
SQ	SEQUENCE 691 AA; 76808 MW; 0BBF06C93F0A3EA0 CRC64;
	Query Match 27.0%; Score 624.5; DB 2; Length 691;
	Best Local Similarity 31.7%; Pred. No. 1.3e-38;
	Matches 136; Conservative 81; Mismatches 169; Indels 43; Gaps 4
QY	10 LCIALALSLAMMTFFRITLLVHIFISLVILGGLFCVGVLMWLYDYDTNDLSIE---- 65
DB	211 VCGLLAISLTATVMHMLSRIVSWIICVLVIVASVALTVKALYAYNIRNKSGVNTQYS 270
QY	66 -LDTERENMKCVLGSFAIVSGITAVLVLVLIPLVKRIKLTVLELFOITNKAISSAPFLLPQ 124
DB	271 MLEEFVRNQAVLTLAVLATITMILIVVIYFLKNKLAGLSALFEELAQCCMMNLPGLLIA 330
QY	125 PLMTFFAILIFFEWLVAVLISLGTAGAA----- 152
DB	331 PLLAFVLIIAFLSFVAVIICTATSPGQSPIAFDNSKAHQQLPANALFVSNSTDVN 390
QY	153 QVMGGQVEYKPLSGIRMYMSYHLIGLIWTSEFILACQOMTIAGAVVTTCYNRSKNDDPPD 212
DB	391 DLRENARVEYADAGVLRSMFWIYYVGLIWTVEFIACQQFALAAAFAWFYFQK----PTS 446
QY	213 HPIUSSLSLFPFYHQGTWVGSGFLISVVRIIPRIIVMYMQNALK--EQHGALSRYLPRCC 270
DB	447 TPTFYALGKLVKHGLTVAKGSFVITTFIKPRLITYLAKLKKGEDKSGSCAACCLKCC 506
QY	271 YCCFWCLDKYLLHLNQNAYYYTTAINGTDFCTSAKDADFKIILSKSSHFTSINCFGDFFIIFL 330
DB	507 ICGFWLLEKFIRFLNNAYTVATESINFPCAGIANMATNVLOVATINSVGFILFL 566
QY	331 GKVLVVCFTVFEGGLMAFNYNRAFGQWAVPLLVAFFAYLVVAHSFLSVFETVDLDAFLCFA 390
DB	567 GKVVVAALSGLIGIVLKKDPGLNFYMAPVYIIIIIFSPFIAHIILSLPEMVVDTLFLCVC 626
QY	391 VDLETNDGS 399
DB	627 EDKTNGRS 635
RESULT 14	
Q9VZE7_DROME	PRELIMINARY; PRT; 691 AA.
AC	Q9VZE7;
DT	01-MAY-2000, integrated into UniProtKB/TREMBL.
DT	21-FEB-2006, entry version 1.
DE	CG1311-PA.
GN	Name=CG1311; ORFNames=Dmel_CGI311;
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_taxid=7227;
RN	[1]
RP	NUCLEOTIDE SEQUENCE.
RX	MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA	Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA	George R.A., Lewis S.J., Richards S., Ashburner M., Henderson S.N.,
RA	Sutton G.G., Wortman J.R., Yeager M.D., Zhang Q., Chen L.X.,
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA	Abriel J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA	Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA	Beeson K.Y., Benos P.V., Bereman B.P., Bhattacharya D., Bolshakov S.,
RA	Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA	Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA	de Pablo B., Delcher A., Deng Z., Duan A.D., Dew I., Dietz S.M.,
RA	Dodson K., Dou P.L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
RA	Furber K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA	Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasse K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Markulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Rubin J.C.:
RT "The genome sequence of *Drosophila melanogaster*.";
RT Science 287:2185-2195 (2000).
RN [2]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champagne M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirkas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Swirskas R., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: release 3 of the *Drosophila*
RT melanogaster euchromatic genome sequence.";
RT Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
RN [3]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J.W., Svirkas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
RT a genomics perspective.";
RT Genome Biol. 3:RESEARCH0084.1-RESEARCH0084.20 (2002).
RN [4]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Battencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
RT systematic review.";
RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22 (2002).
RN [5]

RP NUCLEOTIDE SEQUENCE.
RG Berkeley *Drosophila* Genome Project;
RA Celniker S., Carlson J., Wan K., Pfeiffer B., Frise E., George R.,
RA Hoskins R., Stapleton J., Pacleb J., Park S., Svirkas R., Smith E.,
Yu C., Rubin G.;
RT "Drosophila melanogaster release 4 sequence.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [6]

RP NUCLEOTIDE SEQUENCE.
RG FlyBase;
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
CC -----

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CC
DR EMBL; AE003480; AAF47876.1; -; Genomic DNA.

DR	FlyBase; FBgn0035523; CG1311.
DR	InterPro; IPR007603; DUF580.
DR	PANTHER; PTHR12385; DUF580; 1.
DR	Pfam; PF04515; DUF580; 1.
SQ	SEQUENCE 691 AA; 76840 MW; 73309ED51C733208 CRC64;
Query Match	27.0%; Score 624.5; DB 2; Length 691;
Best local Similarity	31.7%; Pred.No. 1.3e-38;
Matches 136; Conservative	81; Mismatches 169; Indels 43; Gaps 4;
Qy	. 10 LCIALALSAMMFTFRFITTLVHIFISVLGLLFCGVLWLLYYDYTDNLSIE----- 65 :: :: :: :: :: :
Dd	211 VCGALLAISALVTMMHWLSRIVSWIICLVIVASVALTVAWTAYNYNRKNSGVNTQYS 270 :: :: :: :: :: :
Qy	66 -LDTERENMKCVLGFAIVSTGITAVLADLVLFVKRKRIKLVELPQTINKAISSAPFLILFQ 124 :: :: :: :: :: :
Dd	271 MLSEFVRNQAVLTAVLATITMIILVIWVFLKNKLAGLSALPEEAGQCMMNLPGILLIA 330 :: :: :: :: :: :
Qy	125 PLMTFAILIFFWLWLVAVLISLGTAGA------- 152 :: :: :: :: :: :
Dd	331 PLLAFVLIIAFLSFWAVAIICLATASSFGOSPIAPPDPSKAHQOPLPANALFVSNSTDVN 390 :: :: :: :: :: :
Qy	153 QVMEGGOVEYKPLSGIRYMKSHYHLIGLISETFILACQMOTIACAQVTCYNRSKNDPPD 212 :: :: :: :: :: :
Dd	391 DLDPNAKEVDADAGVLRSMFIWIIVUGLIWTVFEIFACQQALAAVAFWFQK----PTS 446 :: :: :: :: :: :
Qy	213 HPILLSLSLFFYHGQTVRVKGSELISVVRIIPRIIMYMONALK--EQOHGALSRYLPFRC 270 :: :: :: :: :: :
Dd	447 TPTFYAIKGLVLYHVGTVAKGSVFITIKPRIILTLYAKLKXGGDKGSCEAACCLKCC 506 :: :: :: :: :: :
Qy	271 YCFWCILDKYLLHNQNAYTTTAINGDTDFCTSAKDAPKIISKNSSHTFSINCFGDIIFL 330 :: :: :: :: :: :
Dd	507 ICGFWILLEKFRLFNHNAYTWVAIESINFCPAAGIANMATNVQLVINSVGDIFILF 566 :: :: :: :: :: :
Qy	331 GKVLVCFTVFGGLMAFYNRAQVMAVPDLLLVAFRAYLAHSFSLSFETVLDALFLCFA 390 :: :: :: :: :: :
Dd	567 GKVVAAALSGILGIYLKKXPGLNFMAPVIIIIIIFSFFIAHIILSFEMVVDILFLCVC 626 :: :: :: :: :: :
Qy	391 VDLETNDS 399
Dd	627 EDKTNGRS 635
RESULT 15	
O6GN42_XENILA	PRELIMINARY; PRT; 707 AA.
ID O6GN42_XENILA	
AC O6GN42_XENILA	
DC 19-JUL-2004,	integrated into UniProtKB/TREMBL.
DT 19-JUL-2004,	sequence version 1.
DT 07-FEB-2006,	entry version 12.
DE MGC83045 protein.	
DN Name=MGC83045;	
OS Xenopus laevis (African clawed frog).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;	
OC Xenopodinae; Xenopus; Xenopus.	
RN NCBI_TaxID=8355;	
OX [1]	
RN NUCLEOTIDE SEQUENCE.	
RP TLSSUB=Embryo;	
KX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,	
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA Diatchenko L., Marasuna K., Farmer A.A., Rubin G.M., Hong L.,	
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,	
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA Villalón D.K., Munzzy D.N., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,	
RA Fahay J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,	

Search completed: June 6, 2006, 22:03:03
Job time : 301 secs

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo;
RC MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]

RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Embryo;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -----

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CC -----

DR EMBL; BC073678; AAH73678.1; -; mRNA.
DR InterPro; IPR007603; DUF580.
DR PANTHER; PTHR12385; DUF580; 1.
DR Pfam; PF04515; DUF580; 1.
SQ SEQUENCE 707 AA; 79320 MW; DCFE8916E17383C1 CRC64;

Query Match 26.4%; Score 611; DB 2; Length 707;
Best Local Similarity 30.5%; Pred. No. 1.4e-37;
Matches 152; Conservative 96; Mismatches 156; Indels 94; Gaps 16;

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Db	228	IITLVIAVMVSLFLILLRFTAGILVWV---LIVGVIGVIG--YGIYHCY-----MEY	276
Qy	67	DTERENMKCV-----LGFAVSTGITAVLLVLFVLKRIKLTVEL	107
Db	277	DTLNKQGVSDVGFTNLGVYPRVKETWLAILLVAVVEAILLVLFLKRLIIAIAL	336
Qy	108	FQITNKAISSAPFLFQPLMTFAILLFFWLWVAVLLSLGTAGA-----AQ	153
Db	337	IKASKAIGHIMSSLFYPLVTFVLLVVCVAYWGMTALYLATSGAPIYRISTVNTSVPGCE	396
Qy	154	VMEGGQ-----VEYKPLSG-----IRYMWIS-----YHLIGLIWTSEFILAC	189
Db	397	NITGNETCNPTFKPSSSCNEARCIFYRYNNEGLFQTNLFNLQIYNYVIGFLWCINFVIAL	456
Qy	190	QQMTIAGAVTCY--FNRSKNDPDHPILSSLSILFFYHOGTVVKGSLISVVRIPRIIV	247
Db	457	GQCVLAGAFASYWAFHKPK-DIPFFVASFMTRLRYHTGSLAFGSLIITVQLIRIIL	515
Qy	248	MYMONALKEOQHGSALRYLFRCCYCCFCWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAF	307
Db	516	EYVDHLKLGAGN-PCTRFLCLCLCCFCWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAF	574
Qy	308	KILSKNSHTSINCFGDFIIFLGKVLVVCFTVFG--GLMAFNY-----NRAFO---	354
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Qy	355	---VWAVPLLLVAFAYLVASHLSVFETVLDAFLCFVADLTNDGSSSEKPYFMDQEFL	411
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Qy	412	SPVKRSNKLNNARAQDQK 429	
Db	689	SILNKNRPPKSEKKKK 706	

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OM protein - protein search, using sw model

Run on: June 6, 2006, 22:03:21 ; Search time 51 Seconds
(without alignments)
763.748 Million cell updates/sec

Title: US-10-063-537-32

Perfect score: 2315

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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- 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
- 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*
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- 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	2315	100.0	445	2	US-09-990-444-177
3	2315	100.0	445	2	US-09-997-333-177
4	2315	100.0	445	2	US-09-992-598-177
5	2315	100.0	445	2	US-09-989-735-177
6	2315	100.0	445	3	US-09-989-726-177
7	2315	100.0	445	3	US-09-997-514-177
8	2315	100.0	445	3	US-09-989-728-177
9	2315	100.0	445	3	US-09-997-349-177
10	2315	100.0	445	3	US-09-997-653-177
11	2315	100.0	445	3	US-09-989-293A-177
12	594.5	25.7	704	2	US-09-547-789-7
13	563	24.3	717	2	US-10-104-047-3465
14	540	23.3	710	2	US-09-547-789-2
15	538.5	23.3	705	2	US-09-547-789-5
16	517	22.3	403	2	US-10-104-047-2454
17	428	18.5	321	2	US-09-991-181-36
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23	428	18.5	321	3	US-09-997-514-36
24	428	18.5	321	3	US-09-989-728-36
25	428	18.5	321	3	US-09-997-349-36
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ALIGNMENTS

RESULT 1

US-09-991-181-177

; Sequence 177, Application US/09991181

; Patent No. 6913919

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; FILE REFERENCE: F27301C53

; CURRENT APPLICATION NUMBER: US/09/991,181

; CURRENT FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/049787

; PRIOR FILING DATE: 1997-06-16

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/065186

; PRIOR FILING DATE: 1997-11-12

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066770

; PRIOR FILING DATE: 1997-11-24

; PRIOR APPLICATION NUMBER: 60/075945

; PRIOR FILING DATE: 1998-02-25

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/083322

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Sequence 166, App
Sequence 166, App
Sequence 4684, Ap
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Sequence 10, Appl
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Sequence 6, Appli

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 ; PRIOR FILING DATE: 1998-07-07
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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

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Db	61	DLSELDTERENMKCVLGFAIVSGITAVLLVLFVLRKRIKLTVELFOITNKAISSAPF	120
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Qy	181	WTSEFIIACQMTAGAVVTCYFNRSKNDPPDPHILSSLSILFFYHOGTVVKGSLISVV	240
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Qy	241	RIPRIIVMYQNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFC	300
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 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Deenoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730P1C19
 ; CURRENT APPLICATION NUMBER: US/09/990,444
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
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 ; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR APPLICATION NUMBER: 60/090694
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2315; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.9e-241;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	DLSEILDTERENMKCVLGFPAIVSTGITAVLLVLI FVLKRKIKLTVELFOITNKAISSAPF	120
Qy	121	LLFQPLWTFAILIFFWLVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMSYHLIGLI	180
Db	121	LLFQPLWTFAILIFFWLVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMSYHLIGLI	180
Qy	181	WTSEFILACQOMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTWVKSFLISVV	240
Db	181	WTSEFILACQOMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTWVKSFLISVV	240
Qy	241	RIPRIIVMYMQUALKEQHQHGSRLFRCCYCCFWCLDKYLLHLNQNAVTTTAINGTDFC	300
Db	241	RIPRIIVMYMQUALKEQHQHGSRLFRCCYCCFWCLDKYLLHLNQNAVTTTAINGTDFC	300
Qy	301	TSAKDAFKILSKNSSHTSINCPGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFOVWAVPL	360
Db	301	TSAKDAFKILSKNSSHTSINCPGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFOVWAVPL	360
Qy	361	LLVAFAYLVVHVSFLSVFETVLDALFLCFADVLETNDGSEKPFYFMDQBFSLSVKSNKL	420
Db	361	LLVAFAYLVVHVSFLSVFETVLDALFLCFADVLETNDGSEKPFYFMDQBFSLSVKSNKL	420
Qy	421	NNARAQQDKHSLRNEEGTGLQAIVR	445
Db	421	NNARAQQDKHSLRNEEGTGLQAIVR	445

RESULT 3
US-09-997-333-177
; Sequence 177, Application US/09997333
; Patent No. 6953836
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C27
CURRENT APPLICATION NUMBER: US/09/997,333
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 1.9e-241;
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QY      1  MSGRDTLGLCIALALSLAMMTFFRITLLVHIFISLVILGLLFCVGLWMLYYDYTN 60
Db      1  MSGRDTLGLCIALALSLAMMTFFRITLLVHIFISLVILGLLFCVGLWMLYYDYTN 60

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Db      121  LLFQPLWTFAILIFFVWLWVAVLLSLGTAGAAQVMGGQVEYKPLSGIRYMWYHILGLI 180

QY      181  WTSEFILACQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILFFYHOGTVVKGSLISVV 240
Db      181  WTSEFILACQMTIAGAVVTCYFNRSKNDDPDHPILSSLSILFFYHOGTVVKGSLISVV 240

QY      241  RIPRIIVMYQNALKEQHQGALSRYLFRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300
Db      241  RIPRIIVMYQNALKEQHQGALSRYLFRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300

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QY      301  TSAKDAFKILSKNSSHFTSINCFDGFIIIFLGKLVVVCFTVFGGLMAFNYNRAQVWAVPL 360
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Db      361  LLVAFAYLVAHSFSLSVFETVLDALFLCFVADLETNDGSEKPYFMDQBFSLSFVKRSNKL 420

QY      421  NNARAQODKHSLSRNEEGTLOAIVR 445
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RESULT 4
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; Sequence 177, Application US/09992598
; Patent No. 6956108
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; PRIOR FILING DATE: 2001-11-14
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; PRIOR APPLICATION NUMBER: 60/087759

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Dd	61	DLSELDTERENKCVLGFAIVSTG	TAVLLVLFVLRKRKLTVVELFOITNKAISSAPP	120						
Qy	121	LLFOPLWTFAILLFFFWLVAVALLSGTAAQWMEGGQVEYKPLSGIRYMWSYHLIGLI	180							
Dd	121	LLFOPLWTFAILLFFFWLVAVALLSGTAAQWMEGGQVEYKPLSGIRYMWSYHLIGLI	180							
Qy	181	WTSEFILACOOMTIAGAVVTCYNFRSKNDPDPHPILSSLSIIFFVHQGTVMKGSLISVV	240							
Dd	181	WTSEFILACOOMTIAGAVVTCYNFRSKNDPDPHPILSSLSIIFFVHQGTVMKGSLISVV	240							
Qy	241	RIPRIIWMYMONALKEQOHGALSRYLCRCYCFCWCCLDKYLHLHNONAYTTTAINGTDTC	300							
Dd	241	RIPRIIWMYMONALKEQOHGALSRYLCRCYCFCWCCLDKYLHLHNONAYTTTAINGTDTC	300							
Qy	301	TSADAPFKILSKNSHSHTSINCGRDFIIFLGKVLVVCFTVFGLMAFNYNRAFAQWAVPL	360							
Dd	301	TSADAPFKILSKNSHSHTSINCGRDFIIFLGKVLVVCFTVFGLMAFNYNRAFAQWAVPL	360							
Qy	361	LLVAFFAYLVAHFSFLSVFEVTLDALFCFAVDLETNDGSSSEKPYFMDOBFSLFVKRSNKL	420							
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RESULT 5										
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; Sequence 177, Application US/09989735										
; Patent No. 6972185										
; GENERAL INFORMATION:										
; APPLICANT: Ashkenazi,Avi J.										
; APPLICANT: Baker,Kevin P.										
; APPLICANT: Botstein,David										
; APPLICANT: Deenoyers,Luc										
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; APPLICANT: Ferrara,Napoleone										
; APPLICANT: Fong,Sherman										
; APPLICANT: Gerber,Hanspeter										
; APPLICANT: Gertsens,Mary E.										
; APPLICANT: Goddard,Audrey										
; APPLICANT: Godowski,Paul J.										
; APPLICANT: Grimaldi,J.Christopher										
; APPLICANT: Gurney,Austin L.										
; APPLICANT: Kijavin,Ivar J.										
; APPLICANT: Napier,Mary A.										
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; APPLICANT: Tumas,Daniel										
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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic										
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; PRIOR FILING DATE: 1998-06-26
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; PRIOR FILING DATE: 1998-06-26

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; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
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; PRIOR APPLICATION NUMBER: 60/09178
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2315; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.9e-241;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSGRDTILGICILALSLAMMFTFRITLLVHIFISLVILGLLFCVGLWMLYYDTN 60
Db 1 MSGRDTILGICILALSLAMMFTFRITLLVHIFISLVILGLLFCVGLWMLYYDTN 60

Qy 61 DLSIELDTERENMKCVLGFPAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPF 120
Db 61 DLSIELDTERENMKCVLGFPAIVSTGITAVLLVLI FVLRKRIKLTVELFQITNKAISSAPF 120

Qy 121 LLFQPLWTFAILFFFWLVWVAVLLSLGTAGAAQMEGGQVEYKPLSGIRYMWVHLLGLI 180
Db 121 LLFQPLWTFAILFFFWLVWVAVLLSLGTAGAAQMEGGQVEYKPLSGIRYMWVHLLGLI 180

Qy 181 WTSEFILACQOMTIAGAVTTCYENRSKNDPPDHPILSSLSILFFYHOGTVVKGSLISV 240
Db 181 WTSEFILACQOMTIAGAVTTCYENRSKNDPPDHPILSSLSILFFYHOGTVVKGSLISV 240

Qy 241 RIPRIIWMYQNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFC 300
Db 241 RIPRIIWMYQNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFC 300

Qy 301 TSAKDAFKILSKNSSHFTSINCFDFFILFLGKLVVVCFTVFGGLMAFNRAFOVAVPL 360
Db 301 TSAKDAFKILSKNSSHFTSINCFDFFILFLGKLVVVCFTVFGGLMAFNRAFOVAVPL 360

Qy 361 LLVAFAYLVAHSFLSVFETVLDALFLCPAVDLETDGSEKPYFMDQEFLSFVKRSNKL 420
Db 361 LLVAFAYLVAHSFLSVFETVLDALFLCPAVDLETDGSEKPYFMDQEFLSFVKRSNKL 420

Qy 421 NNARAQODKHSRNEEGTELQAIVR 445
Db 421 NNARAQODKHSRNEEGTELQAIVR 445

RESULT 6
US-09-989-726-177
; Sequence 177, Application US/09989726
; Patent No. 7018811
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney,Austin L.
; APPLICANT: KJavin,Ivar J.
; APPLICANT: Napier,Mary A.
; APPLICANT: Pan,James
; APPLICANT: Paoni,Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1660
; CURRENT APPLICATION NUMBER: US/09/989,726
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
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34 PRIOR APPLICATION NUMBER: 60/091978
35 PRIOR FILING DATE: 1998-07-07
36 PRIOR APPLICATION NUMBER: 60/091982
37 PRIOR FILING DATE: 1998-07-07
38 PRIOR APPLICATION NUMBER: 60/092182
39 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2315; DB 3; Length 445;
Best Local Similarity 100.0%; Pred. No. 1.9e-241; Mismatches 0; Indels 0; Gaps 0;
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DB 61 DLSIELDTERENKCVLGFPAIVSTGITAVALLVILFVLRKIKLTVLFOITNKAISSAPF 120
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DB 121 LLFQPLMTFAILIFFVWLWAVLLSLCTAGAAQWMEGGQVEYKPLSGIRYVWWSYHLIGLI 180
QY 181 WTSEFILACQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQTGVVKSFLISVV 240
DB 181 WTSEFILACQMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQTGVVKSFLISVV 240
QY 241 RIPRIIWMQNALKEQHGALSRYLPRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300
DB 241 RIPRIIWMQNALKEQHGALSRYLPRCCYCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300
QY 301 TSARDAFKILSKSSHETSINCGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVAVPL 360
DB 301 TSARDAFKILSKSSHETSINCGDFIIFLGKVLVVCFTVFGGLMAFNYNRAQVAVPL 360
QY 361 LLVAFFAYLVHAFSLVSFVETVLDALFLCFADVLETDNGSSEKPYFMDQDFLSFKRSNKL 420
DB 361 LLVAFFAYLVHAFSLVSFVETVLDALFLCFADVLETDNGSSEKPYFMDQDFLSFKRSNKL 420
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Db 421 NNARAQODKHSRLNEEGTELQAIVR 445
RESULT 7
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; Sequence 177, Application US/09997514
; Patent No. 7019116
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deanoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C46
; CURRENT APPLICATION NUMBER: US/09/997,514
; CURRENT FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
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; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
; PRIOR FILING DATE: 1998-05-28
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; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088026
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028

Qy 121 LLFQPLWTFALLIFFWLWVAVILSLGTAGAAQWMEGQVEYKPLSGIRYMWSYHLIGLI 180
Db 121 LLFQPLWTFALLIFFWLWVAVILSLGTAGAAQWMEGQVEYKPLSGIRYMWSYHLIGLI 180
Qy 181 WTSFILLACQOMTITAGAVVTCYFNRSKNDPPDHPILSSLSILFFVHQTGVVKGSLISVW 240
Db 181 WTSFILLACQOMTITAGAVVTCYFNRSKNDPPDHPILSSLSILFFVHQTGVVKGSLISVW 240
Qy 241 RIPRIIVVMQNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAAYTTTAINGTDFC 300
Db 241 RIPRIIVVMQNALKEQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAAYTTTAINGTDFC 300
Qy 301 TSAKDARKILSKNSHSTINCFGDFIIFLGKVLVWCFTVFGGLMAFNYNRAFOVWAVPL 360
Db 301 TSAKDARKILSKNSHSTINCFGDFIIFLGKVLVWCFTVFGGLMAFNYNRAFOVWAVPL 360
Qy 361 LLVAFAYLVVAHSFLSFVETVLDALFLCFAVDLETDGSSSKPYFMDQEFLSFVKRSNKL 420
Db 361 LLVAFAYLVVAHSFLSFVETVLDALFLCFAVDLETDGSSSKPYFMDQEFLSFVKRSNKL 420
Qy 421 NNARAQQDKHSRNEEGTELQAIVR 445
Db 421 NNARAQQDKHSRNEEGTELQAIVR 445

RESULT 8

US-09-989-728-177
; Sequence 177, Application US/09989728
; Patent No. 7029873
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C72
; CURRENT APPLICATION NUMBER: US/09/989,728
; CURRENT FILING DATE: 2001-11-20
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
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; PRIOR APPLICATION NUMBER: 60/075945
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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

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Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 241 RIPRIIVMYMQLKEQHQHGLSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFC 300
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Qy 301 TSADAFKILSKNSHFTSINCFCDFIIFLGKVLVVCFTVFGGLMAFNRAFOQWAVPL 360
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; Sequence 177, Application US/09997349
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; GENERAL INFORMATION:
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; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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; PRIOR FILING DATE: 1998-07-09

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RESULT 10

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; APPLICANT: Ashkenazi, Avi J.

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; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2315; DB 3; Length 445;

Best Local Similarity 100.0%; Pred. No. 1.9e-241;

Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSGRDITLGLCIIALALSLAMMFTFITTLLVHIFISLVILGLLFCVGLWMLYYDTN	60
Db	1	MSGRDITLGLCIIALALSLAMMFTFITTLLVHIFISLVILGLLFCVGLWMLYYDTN	60
Qy	61	DLSELDTERENMKCVLGFPAIVSTGTTAVLLVLFVLRKRIKLTVELFQITNKAISSAPP	120
Db	61	DLSELDTERENMKCVLGFPAIVSTGTTAVLLVLFVLRKRIKLTVELFQITNKAISSAPP	120
Qy	121	LLFQPLMTFAILLFFVWLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLI	180
Db	121	LLFQPLMTFAILLFFVWLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLI	180
Qy	181	WTSEFILACQOMTIAGAVTTCYFNRSKNDDPPDHPILSSLSILFFYHOGTVVKGSLISVV	240
Db	181	WTSEFILACQOMTIAGAVTTCYFNRSKNDDPPDHPILSSLSILFFYHOGTVVKGSLISVV	240
Qy	241	RIPRIIWMYMONALKEQHGLSRVLPCCYCCFCWCLDKYLLHNLONAYTTTALNGTDFC	300

Db 241 RIPRIIVVMQNALKEQHGALSRYLPRCCVCCFWCLDKYLLHLNQNAVYTTTAINGTDFC 300
Qy 301 TSAKDAFKILSKSSHSTINCGDFIIFLGKVLVWCFTYVFGGIMAFNRYRAFQVWAVPL 360
Db 301 TSAKDAFKILSKSSHSTINCGDFIIFLGKVLVWCFTYVFGGIMAFNRYRAFQVWAVPL 360
Qy 361 LLVAFFAYLVHVSFLSVFETVLDALFLCFAVDLETNDSSEKPYFMDQEFLSFVKRSNKL 420
Db 361 LLVAFFAYLVHVSFLSVFETVLDALFLCFAVDLETNDSSEKPYFMDQEFLSFVKRSNKL 420
Qy 421 NNAAQODKHSLSRNEETELQAIVR 445
Db 421 NNAAQODKHSLSRNEETELQAIVR 445

RESULT 11
US-09-989-293A-177
; Sequence 177, Application US/09989293A
; Patent No. 7034136
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C66
; CURRENT APPLICATION NUMBER: US/09/989, 293A
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066770
; PRIOR FILING DATE: 1997-11-24
; PRIOR APPLICATION NUMBER: 60/075945
; PRIOR FILING DATE: 1998-02-25
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/083322
; PRIOR FILING DATE: 1998-04-28
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/087106
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; PRIOR APPLICATION NUMBER: 60/087609
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; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088021
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-04
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; PRIOR FILING DATE: 1998-06-05
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; PRIOR APPLICATION NUMBER: 60/089105
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; PRIOR APPLICATION NUMBER: 60/089512
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; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089801
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089907
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; PRIOR APPLICATION NUMBER: 60/089908

; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090862
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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091544
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 2315; DB 3; Length 445;

Best Local Similarity 100.0%; Pred. No. 1.9e-241;
Matches 445; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSGRDTILGICILALALSLAMMFTFRITLLVHIFISLVILGLLFFVCGVLMWLYDYDTN 60
Db 1 MSGRDTILGICILALALSLAMMFTFRITLLVHIFISLVILGLLFFVCGVLMWLYDYDTN 60
Qy 61 DLSIELDTERENMKCVLGFPAIVSTGITAVLLVLFVLRKRIKLTVELFQITNKAISSAPP 120
Db 61 DLSIELDTERENMKCVLGFPAIVSTGITAVLLVLFVLRKRIKLTVELFQITNKAISSAPP 120
Qy 121 LLFQPLWTFPAILIFFFWLVAVLLSLGTAGAAQMEGGQVEYKPLSGIRYMWVSHLGLI 180
Db 121 LLFQPLWTFPAILIFFFWLVAVLLSLGTAGAAQMEGGQVEYKPLSGIRYMWVSHLGLI 180
Qy 181 WTSEFILACQOMTIAGAVVTCYFNRSKNDDPPDHPILSSLSILFFYHGTGVVKGSLISVV 240
Db 181 WTSEFILACQOMTIAGAVVTCYFNRSKNDDPPDHPILSSLSILFFYHGTGVVKGSLISVV 240
Qy 241 RIPRIIWMYQNALKEQOQHGALSRYLPRCCYCCFWCLDKYLLHLNQNAYTITTAINGTDFC 300
Db 241 RIPRIIWMYQNALKEQOQHGALSRYLPRCCYCCFWCLDKYLLHLNQNAYTITTAINGTDFC 300
Qy 301 TSAKDAPKILSKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNRAFOVWAVPL 360
Db 301 TSAKDAPKILSKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNRAFOVWAVPL 360
Qy 361 LLVAFAYLVVHVSFLSVFETVLDALFLCFVAVDLETNDGSSEKPYFMDQEFLSFVKRSNKL 420
Db 361 LLVAFAYLVVHVSFLSVFETVLDALFLCFVAVDLETNDGSSEKPYFMDQEFLSFVKRSNKL 420
Qy 421 NNARAQODKHSRLNEEGTELOAIVR 445
Db 421 NNARAQODKHSRLNEEGTELOAIVR 445

RESULT 12

US-09-547-789-7
; Sequence 7, Application US/09547789
; Patent No. 6943235
; GENERAL INFORMATION:
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; TITLE OF INVENTION: NOVEL 13-TRANSMEMBRANE PROTEIN EXPRESSED
; FILE REFERENCE: 129.11USU1
; CURRENT APPLICATION NUMBER: US/09/547,789
; CURRENT FILING DATE: 2000-04-12
; EARLIER APPLICATION NUMBER: 60/128,858
; EARLIER FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 704
; TYPE: PRT
; ORGANISM: Human
US-09-547-789-7

Query Match 25.7%; Score 594.5; DB 2; Length 704;
Best Local Similarity 30.1%; Pred. No. 4e-55;
Matches 147; Conservative 90; Mismatches 153; Indels 99; Gaps 15;
Qy 7 ILGICILALALSLAMMFTFRITLLVHIFISLVILGLLFFVCGVLMWLYDYDTN--- 60
Db 234 IIGL-VIAMAMSLFLILRLFLAGIMVWMVIMVILVGLGIFHC-----YMEISLRG 286
Qy 61 -----DLSIELDTE-----RNNMKCVLGFPAIVSTGITAVLLVLFVLRKRIKLTVE 106
Db 287 EAGSDVSLVDLGFQTDPRVVLHLRQIW---LAPWILSILEVILLILFLRKLITAI 343

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QY 107 LFOITNKAISSAPPELLPOPLWTFATILFFWVLWVAVLLSLGTAGAAQ----- 153
| : : : | | | | | : : : | : : : |
Db 344 LIKEASRAGVVMCSLLYPLVTFLLCLCLAYWASTAVFLSTNEAVYKIFDDSPCPFTA 403
| : : : | | | | | : : : | : : : |
QY 154 -----VMEGGQVEY-KPLSGIRYMWVSYHLIGLIWTSBFILA 188
| : : : | | | | | : : : | : : : |
Db 404 KTCNPETFPSSHESROCPNARCOQVFGSGVHRALLGLQI---FNAPFFWLANFVLA 460
| : : : | | | | | : : : | : : : |
QY 189 CQOMTAGAVVTCYFN-RSKNDPDPHIPILSSLSILFFYHOGTVVKGSLISVVRIPRIIV 247
| : : : | | | | | : : : | : : : |
Db 461 LGQVTLTAGAFASYWALRKDDLPAPFLSFAFGRALRYHTGSLAFGALILAIQIIRVIL 520
| : : : | | | | | : : : | : : : |
QY 248 MYMONALKEOQHGAISRYLPRCCVCCFWCLDKYLLHLNONAYTTTAINGDTFCTSAKDAF 307
| : : : | | | | | : : : | : : : |
Db 521 EYLDQRLKAEN-KFAKCLMTCLKCCFCWCLEKIKFLNRNAYIMAIYGNFCTSRNAF 579
| : : : | | | | | : : : | : : : |
QY 308 KILSKNSSHFTSINCFGDFIFIIGKVLVWCFTVFGGLMAF-----NYN 350
| : : : | | | | | : : : | : : : |
Db 580 FLLMRNIIRVAVLDKVDLDFLLGKLLVGSV---GILAPFFTHRIRIVQDTAPPLNY- 635
| : : : | | | | | : : : | : : : |
QY 351 RAFQWAVPILLIYAFAYLVHAFSLVSFETVLDALFLCPAVDLETNDGSEKSEKPYMDQEF 410
| : : : | | | | | : : : | : : : |
Db 636 ----YV-VPLTVIVGSYLIAGHFFSVYGMCDVTLFCFLLEDLRNDGSAERPFFMSSTL 690
| : : : | | | | | : : : | : : : |
QY 411 LSPVKRSNK 419
| : : : |
Db 691 KLLNKNTNK 699
| : : : |
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RESULT 13

US-10-104-047-3465

; Sequence 3465, Application US/10104047

; Patent No. 6943241

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: No. 6943241el full length cDNA

; FILE REFERENCE: H1-A0105

; CURRENT APPLICATION NUMBER: US/10/104,047

; PRIOR FILING DATE: 2002-03-25

; PRIOR FILING DATE:

; NUMBER OF SEQ ID NOS: 4096

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3465

; LENGTH: 717

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-104-047-3465

Query Match

24.3%; Score 563; DB 2; Length 717;

Best Local Similarity 29.7%; Pred. No. 1.1e-51;

Matches 142; Conservative 87; Mismatches 171; Indels 78; Gaps 14;

QY 7 ILGLCILALSLAMMFTFRFITLLVHIFISVLGLLFCVGV-LWMLYYDYN----- 60

| : : : | | | | | : : : | : : : |

Db 246 LIGLTI-AMVLSWIFLLRFLRFIAGCLFWF---MIGVIGIYGWHCVQOYTNLQEP 300

| : : : | | | | | : : : | : : : |

QY 61 -----DLSIEDTER--ENMKCVLGFPAIVSGITAVLLVLFVLRKIKLTVLFPQIT 111

| : : : | | | | | : : : | : : : |

Db 301 SSVLTIIYDIGIOTNISMYPELOQTWTFEMIILCIIEVILMILFLENRIRVAIILKEG 360

| : : : | | | | | : : : | : : : |

QY 112 NKAISSAPPELLFOPLMTFATILFFWVLWVAVLLSLGTAGA----- 151

| : : : | | | | | : : : | : : : |

Db 361 SKAIGVPTLVYPAITFILLSICICYWVVVAVFLATSGVPVYKVYAPGGCHIHENQTC 420

| : : : | | | | | : : : | : : : |

QY 152 -----AQVMEGGQVEYKPLSG-----IRYMWVSYHLIGL-----IWTSEFILACQOMTIA 195

| : : : | | | | | : : : | : : : |

Db 421 PEIFNTETIAKACPGALCNFAFYGKSLYHQIYPTFHVYVNLVFLWLNLFVIALGQCALA 480

| : : : | | | | | : : : | : : : |

QY 196 GAVVTCYFNRSK-NDPDPHPILSSLSILFFYHOGTVVKGSLISVVRIPRIIVMYNQAL 254

| : : : | | | | | : : : | : : : |

Db 481 GAFATYVWAMKPPDDIPRYPPPTAFGRATRYHTGSLAFGSLIILAIQMFKIVLEYLDHRL 540

| : : : | | | | | : : : | : : : |

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QY 255 KEQOQHGAISRYLPRCCVCCFWCLDKYLLHLNONAYTTTAINGDTFCTSAKDAFKILSKNS 314
| : : : | | | | | : : : | : : : |
Db 541 KRTQN-TLSKFLQCCRCFCWCLENAIKFLNRNAYIMAIYGNFCRSKADAFNLLMRNV 599
| : : : | | | | | : : : | : : : |
QY 315 SHFTSINCFGDFIFIIGKVLV-----VCFT-----VFGGLMAFNYNRAPQWAVPL 360
| : : : | | | | | : : : | : : : |
Db 600 LKVAVTDVETVYFLFLGKLLVAGSIGVLAFLFTQRLPVIAQGPASLNY-----YV-VPL 653
| : : : | | | | | : : : | : : : |
QY 361 LLVAFAYLVHAFSLVSFETVLDALFLCPAVDLETNDGSEKSEKPYMDQEFLSFVKRSN 418
| : : : | | | | | : : : | : : : |
Db 654 LTVIFGSYLIAGHFFSVYAMCVETIPICFLEDLRNDGSTARPYVVSQPLLKIFOBEN 711
| : : : | | | | | : : : | : : : |
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RESULT 14

US-09-547-789-2

; Sequence 2, Application US/09547789

; Patent No. 6943235

; GENERAL INFORMATION:

; APPLICANT: Daniel E.H. Afar

; APPLICANT: Rene S. Hubert

; APPLICANT: Kahan Leong

; APPLICANT: Arthur B. Raitano

; APPLICANT: Douglas C. Saffran

; TITLE OF INVENTION: NOVEL 13-TRANSMEMBRANE PROTEIN EXPRESSED

; FILE REFERENCE: 129.11USU1

; CURRENT APPLICATION NUMBER: US/09/547,789

; EARLIER APPLICATION NUMBER: 60/128,858

; EARLIER FILING DATE: 1999-04-12

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 710

; TYPE: PRT

; ORGANISM: Human

US-09-547-789-2

Query Match

23.3%; Score 540; DB 2; Length 710;

Best Local Similarity 28.0%; Pred. No. 3.2e-49;

Matches 135; Conservative 98; Mismatches 160; Indels 90; Gaps 14;

QY 12 ILALALSAMMFTFRFITLLVHIFISVLGLLFCVGV-LWMLYY----- 56

| : : : | | | | | : : : | : : : |

Db 233 LVALGVALVLSLLFILLRLVAGPLVLLVGLV---GVLAYGIYVWEYRVLRLDKGAS 289

| : : : | | | | | : : : | : : : |

QY 57 ----DYTNDSLIEDTERENMKCVLGFPAIVSGITAVLLVLFVLRKIKLTVLFPQITN 112

| : : : | | | | | : : : | : : : |

Db 290 ISQLGFTTNLSAYQSVOETWLAALIVLAV---LEAILLLMLIFLQRIRIALLKKEAS 345

| : : : | | | | | : : : | : : : |

QY 113 KAISSAPPELLFOPLMTFATILFFWVLWVAVLLSLGTAG-----AAQVMEGGQVEYKPL 165

| : : : | | | | | : : : | : : : |

Db 346 KAVGQMMSTMFPLVTFVLLLCIAWAWTALYATSGOPQVVLWASNISSPG-CEKVP 404

| : : : | | | | | : : : | : : : |

QY 166 S-----GIRYMWV-----YHLIGLIMTSEFILACQOMT 193

| : : : | | | | | : : : | : : : |

Db 405 NTSNCPHTAHNVSSCPGLMVCVFGYSSKGLIORSVFNLIQYVGLGLFWLWVLAALGQCV 464

| : : : | | | | | : : : | : : : |

QY 194 IGAVVTCYFNRSK-NDPDPHPILSSLSILFFYHOGTVVKGSLISVVRIPRIIVMYMON 252

| : : : | | | | | : : : | : : : |

Db 465 LAGAFASFYWAFHKPODITFPLISAFIRTLRYHTGSLAFGALILTLVQIARVILEYIDH 524

| : : : | | | | | : : : | : : : |

QY 253 ALKEOQHGAISRYLPRCCVCCFWCLDKYLLHLNONAYTTTAINGDTFCTSAKDAFKILSK 312

| : : : | | | | | : : : | : : : |

Db 525 KURGVQN-PVACIMCCFKCLWCLKEKFKFLNRNAYIMAIYGNFCRSKADAFNLLMR 583

| : : : | | | | | : : : | : : : |

QY 313 NSSHFTSINCFGDFIFIIGKVLV-----CFTVFGGLMA-----FNYNRAFQVW 356

| : : : | | | | | : : : | : : : |

Db 584 NIVRVVVLVDKVTDLFLFGKLLVGVGVLSFFFFSGRIPGLGKDFKPSHLNY-----YV 638

| : : : | | | | | : : : | : : : |

QY 357 AVPLLVAFAFAYLVHAFSLVSFETVLDALFLCPAVDLETNDGSEKSEKPYMDQEFLSFVKR 416

| : : : | | | | | : : : | : : : |

Db 639 -LPIMTSILGAYVIASGFFSVFGMCDVTLFLCFLLEDLRNNGSLDRPYVMSKSLKILGK 697

| : : : | | | | | : : : | : : : |

Job time : 53 secs

Qy 417 SNK 419
|:
Db 698 KNE 700

RESULT 15
US-09-547-789-5
; Sequence 5, Application US/09547789
; Patent No. 6943235
; GENERAL INFORMATION:
; APPLICANT: Daniel E. H. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; TITLE OF INVENTION: NOVEL 13-TRANSMEMBRANE PROTEIN EXPRESSED
; FILE REFERENCE: 129.11USUI
; CURRENT APPLICATION NUMBER: US/09/547,789
; CURRENT FILING DATE: 2000-04-12
; EARLIER APPLICATION NUMBER: 60/128,858
; EARLIER FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 705
; TYPE: PRT
; ORGANISM: Mouse
US-09-547-789-5

Query Match 23.3%; Score 538.5; DB 2; Length 705;
Best Local Similarity 27.7%; Pred. No. 4.6e-49;
Matches 133; Conservative 87; Mismatches 174; Indels 87; Gaps 9;
Qy 12 ILALALSAMMFFRFTITLLVHIFISLVILGLLFVC--GVL-WWLYDYDNDLSIELDT 68
Db 229 LVALGVALSLGLFILLRLVAAPLVLLVGLVAVLAYGIYHCWQQYQVFRDKGASITQ 288
Qy 69 ERENMKCVLGFA-----IVSTGITAVLLVLPVLRKRIKLTVELFQIT 111
Db 289 -----LQFTNFSAYQSVKETWLAALIVLAVLEGILLMLLIFLQRIALKEA 340
Qy 112 NKAISSAPFLLOPLWTFAILIFFWVLWVAVLLSLGTAGAAQ----- 153
Db 341 SRAVGQMMSTMFPLVTFVLLVICIGYNAVLTALYATSGQPQIYMASNTSTPCENVPV 400
Qy 154 -----VMEGQVEYKPLSGIRYMWVSYHLGLIWTSEFILACQMTI 194
Db 401 NMTCDPMAPLNSCPNLKCVFKGYSTTGLAQRSLFNLOIYGVGLFWTVNVLALGQCVL 460
Qy 195 AGAVVTCYFNRSK-NDPPDHPILSSLSILFFYHOGTVVKGSLISVVRIPIIIVMYMNA 253
Db 461 AGAFASYFAFHKPRDIPTPPLSSAPFTRLYHTGSLAFGALISLVQIARVILEYIDHK 520
Qy 254 LKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAVTTTAINGTDFCTSAKDAFKILSKN 313
Db 521 LRGSQN-PVARTICCFKCLWCLEKFIKFLNRNAYIMAIYGNFCVSAKNAFMLLRN 579
Qy 314 SSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNY-----NRAFQWAV 358
Db 580 VLRVVLVDKVTDLALLFFGKLLV-----GGVGVLSFFFSGRIKGLGKDFENPNLYWL 634
Qy 359 PLLLVAFAYLVAAHSPVLSVFETVLDAFLCFADVLETDNDGSEKPYEMDOEFLSFVKRSN 418
Db 635 PIMTSINGAIVIASGFFSVGMCMVDTLFLCFLEDLERNDSQERPYNPKALLKILGKN 694
Qy 419 K 419
Db 695 E 695

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